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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:54 ; Search time 158.26 Seconds  
(without alignments)  
4.211 Million cell updates/sec

Title: US-09-723-197-5  
Perfect score: 35  
Sequence: 1 RYIHP 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues 747574  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

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2:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
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9:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
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16:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
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19:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	17	AA95666
2	35	100.0	6	19	AAW65601
3	35	100.0	6	19	AAW64732
4	35	100.0	6	19	AAW71114
5	35	100.0	6	19	AAW65540
6	35	100.0	6	20	AAW49590
7	35	100.0	6	20	AAW33905
8	35	100.0	6	20	AAW30543
9	35	100.0	6	20	AAW30587
10	35	100.0	6	20	AAW32718
11	35	100.0	6	20	AAW33772

12	35	100.0	6	20	AAW15349	Angiotensin II (AI
13	35	100.0	6	20	AAW15309	Angiotensin II (AI
14	35	100.0	6	21	AAW27405	Angiotensin II ana
15	35	100.0	6	21	AAW28103	Angiotensin II ana
16	35	100.0	6	21	AAW84128	Peptide comprising
17	35	100.0	6	21	AAW77041	Angiotensin II (AI
18	35	100.0	6	21	AAW57405	Angiotensin peptid
19	35	100.0	6	22	AAE08875	AII peptide (resid
20	35	100.0	6	22	AAE02992	Human angiotensin
21	35	100.0	6	22	AAE03155	Human angiotensin
22	35	100.0	6	22	AAW91487	Angiotensin peptid
23	35	100.0	7	2	AAPI0431	Angiotensin II oct
24	35	100.0	7	16	AAW87681	Angiotensin III fo
25	35	100.0	7	17	AAW95665	Angiotensin II fra
26	35	100.0	7	17	AAW95663	Angiotensin II fra
27	35	100.0	7	18	AAW33318	Targetting conjuga
28	35	100.0	7	18	AAW33010	Targetting conjuga
29	35	100.0	7	18	AAW11202	Conjugating peptid
30	35	100.0	7	18	AAW14976	Angiotensin II ana
31	35	100.0	7	19	AAW65598	Angiotensin II ana
32	35	100.0	7	19	AAW65600	Angiotensin II ana
33	35	100.0	7	19	AAW64729	Angiotensin II pep
34	35	100.0	7	19	AAW64731	Angiotensin II pep
35	35	100.0	7	19	AAW65633	Angiotensin III an
36	35	100.0	7	19	AAW65641	Angiotensin III an
37	35	100.0	7	19	AAW71111	Peptide AII(2-8) u
38	35	100.0	7	19	AAW71113	Peptide AII(1-7) u
39	35	100.0	7	20	AAW49587	Angiotensin analog
40	35	100.0	7	20	AAW49589	Angiotensin analog
41	35	100.0	7	20	AAW50296	Neutrophil-activat
42	35	100.0	7	20	AAW50298	Neutrophil-activat
43	35	100.0	7	20	AAW33902	Angiotensin II ana
44	35	100.0	7	20	AAW33904	Angiotensin II ana
45	35	100.0	7	20	AAW30540	Amino acid sequenc

#### ALIGNMENTS

RESULT 1

AA95666

ID AA95666 standard; peptide; 6 AA.

XX

AC

AA95666;

XX

DT 09-JAN-1997 (first entry)

XX

Angiotensin II fragment AII(2-7).

XX

Angiotensin II; AII2; vasoconstrictor; arteriole; angiotensin; renin;

KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;

KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.

XX

Synthetic.

XX

PN WO9614858-A1.

XX

PD 23-MAY-1996.

XX

PF 14-NOV-1995; 95WO-US14764.

XX

PR 06-JUN-1995; 95US-0465775.

XX

PR 14-NOV-1994; 94US-0337781.

XX

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX

PI Peptide AII(2-7) u

XX

PI Peptide motif havi

XX

Angiotensin analog

DR

Angiotensin II ana

XX

Amino acid sequenc

PT

Accelerating wound healing by application of angiotensin II

PT fragments - are effective at very low concn. and do not cause

PT hypertension

XX Disclosure; Page 4; 46pp; English.

XX

CC AAR95663-R95672 represent fragments of angiotensin II (AT2).. AT2 (see

CC AAR95662) is an octapeptide present in humans and other species. AT2 is

CC one of the most potent vasoconstrictors known, causing constriction of

CC the arterioles. The formation of angiotensin is initiated by the action

CC of renin on angiotensinogen. The substance formed is a decapeptide

CC called angiotensin I which is converted by the enzyme angiotensinase (by

CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release

CC of extracellular matrices involved in wound repair. These fragments can

CC be used in a compound for accelerating wound healing. The compounds are

CC administered as matrix or micellar solutions, formulated with a

CC carrier or diluent, alternatively the compound is applied in conjunction

CC with a wound dressing. The carrier used in the composition is

CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly

CC glycols. By using fragments of this sequence (or analogues of it),

CC growth as well as healing of tissues is improved, such as in cases of

CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or

CC intraperitoneal surgical wounds. The compounds containing the AT2

CC fragments are less hypertensive than full length AT2, and are also

CC effective at much lower (nanomolar) concentrations than full length AT2.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIYHP 6  
 |||||  
 Db 1 rvyihp 6

## RESULT 2

AAW65601  
 ID AAW65601 standard; peptide; 6 AA.  
 XX  
 AC AAW65601;  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Angiotensin II analogue, AII(2-7).  
 XX  
 KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;  
 KW wound healing.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9826795-A1.  
 XX  
 PD 25-JUN-1998.  
 XX  
 PF 16-DEC-1997; 97WO-US23461.  
 XX  
 PR 15-DEC-1997; 97US-099066A.  
 PR 16-DEC-1996; 96US-0028310.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Dizerega GS, Rodgers KE;  
 XX  
 DR WPI; 1998-362518/31.  
 XX  
 PT Promoting incorporation of skin graft onto underlying tissue -  
 PT comprises pre-treating graft with angiotensin II, or analogue or  
 PT peptide fragment  
 XX  
 PS Disclosure; Page 6; 82pp; English.  
 XX  
 CC The invention relates to the use of angiotensin II (AII), AII analogues,

CC AII fragments and AII fragment analogues for promoting incorporation of a

CC skin graft into underlying tissue of a mammal. The peptides are effective

CC in accelerating the growth or healing of skin grafts and in accelerating

CC re-epithelialisation and tissue repair, even at very low concentrations.

CC They can significantly accelerate the rate of healing at nanomolar levels

CC in vivo. AII accelerates wound repair by increased neovascularisation,

CC growth factor release, re-epithelialisation, extracellular matrix production

CC and increased flow of blood and nutrients to the injured tissue. Use of

CC the above peptides other than AII itself (an extremely potent vaso-

CC constrictor) may avoid the side-effects of AII, such as an increase in blood

CC pressure and thirst. The present sequence represents an angiotensin

CC II fragment.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIYHP 6  
 |||||  
 Db 1 rvyihp 6

## RESULT 3

AAW64732  
 ID AAW64732 standard; peptide; 6 AA.  
 XX  
 AC AAW64732;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE Angiotensin II peptide #4.  
 XX  
 KW Proliferation; mesenchymal stem cell; lineage-specific cell;  
 KW haematopoietic; cell culture; transplantation; treatment; malignant;  
 KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9832457-A2.  
 XX  
 PD 30-JUL-1998.  
 XX  
 PF 26-JAN-1998; 98WO-US01552.  
 XX  
 PR 23-JAN-1998; 98US-0066593.  
 PR 28-JAN-1997; 97US-0036507.  
 PR 08-MAY-1997; 97US-0046859.  
 PR 28-OCT-1997; 97US-0063684.  
 PR 31-OCT-1997; 97US-0063910.  
 PR 18-NOV-1997; 97US-0065612.  
 PR 26-NOV-1997; 97US-0066593.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI dizerega G, Rodgers KE;  
 XX  
 DR WPI; 1998-437044/37.  
 XX  
 PT Promoting haematopoietic and mesenchymal cell proliferation and  
 PT differentiation - by contacting the cells with angiotensinogen,  
 PT angiotensin I or II, or analogues or fragments of these

Claim 7; Page 14; 114pp; English.

AAW64728-W64763 are peptides used in a novel method for accelerating the

proliferation of mesenchymal stem cells (MSCs), haematopoietic

lineage-specific cells or mesenchymal lineage-specific cells. The method

involves contacting the cells with an active agent comprising a sequence

consisting of at least three contiguous amino acids of groups R1-R8 in



CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together  
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptidic group, R3 = Val,  
CC Ala, Leu, norLeu, Ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane  
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoSer or  
CC azarTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or  
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are  
CC not defined in the specification, the peptide bond between Ra and Rb is  
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a  
CC terminal Tyr group. A second active agent comprising a sequence  
CC consisting of at least three contiguous amino acids of groups R2-R8 in  
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,  
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also  
CC described. The inventions are particularly useful in cell culture  
CC mediums. These cells may be used in transplantation techniques for  
CC treatment of malignant or inherited diseases. The formulae represent  
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),  
CC or AII AT2 type 2 receptor agonists.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVYIHP 6  
|||||  
Db 1 rvyihp 6

RESULT 4  
AAW71114  
ID AAW71114 standard; peptide; 6 AA.

XX AC AAW71114;

XX DT 27-OCT-1998 (first entry)

XX DE Peptide AII(2-7) used to accelerate thermal wound healing.

XX KW Angiotensin; AII; acceleration; thermal wound healing; human;  
XX growth factor release; neovascularisation; re-epithelialisation;  
XX extracellular matrix production.

XX OS Synthetic.

XX PN WO9833813-A2.

XX PD 06-AUG-1998.

XX PF 04-FEB-1998; 98WO-US02049.

XX PR 04-FEB-1997; 97US-0037166.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX DR WPI; 1998-437391/37.

XX PT Methods for accelerating thermal wound healing in humans - using  
XX angiotensinogen II and AII analogues

XX PS Claim 3; Page 9; 58pp; English.

XX CC AAW71110-27 represent peptide used in the method of the invention. The  
XX specification describes a method of accelerating thermal wound healing  
XX in humans. The method comprises applying to the thermally injured tissue  
XX an amount of at least one active agent which comprises the peptides  
XX AAW71115-27. The method can be used to promote the healing of thermal  
XX wounds by accelerating growth factor release, neovascularisation,  
XX re-epithelialisation and extracellular matrix production. The sequences  
XX are analogues of the angiotensin or angiotensinogen family of proteins.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVYIHP 6  
|||||  
Db 1 rvyihp 6

RESULT 5  
AAW65540  
ID AAW65540 standard; peptide; 6 AA.

XX AC AAW65540;

XX DT 12-OCT-1998 (first entry)

XX DE Peptide motif having affinity for angiotensin II receptor.

XX KW Endothelin-1; angiotensin II receptor; imaging; cardiovascular disease;  
XX losartan; contrast medium; diagnosis; lanthanide; biotin; lipopeptide;  
XX KW fibrin-anti-polymerant peptide; motif.

XX OS Synthetic.

XX PN WO9818496-A2.

XX PD 07-MAY-1998.

XX PF 28-OCT-1997; 97WO-GB02956.

XX PR 24-MAR-1997; 97GB-0006063.

XX PR 28-OCT-1996; 96GB-0022364.

XX PR 28-OCT-1996; 96GB-0022365.

XX PR 28-OCT-1996; 96GB-0022366.

XX PR 28-OCT-1996; 96GB-0022367.

XX PR 28-OCT-1996; 96GB-0022368.

XX PR 15-JAN-1997; 97GB-0000699.

XX PR 04-FEB-1997; 97GB-0002195.

XX PA (COCK/) COCKBAIN J.

XX PA (NYCO-) NYCOMED IMAGING AS.

XX PI Cuthbertson A, Klaveness J, Naevestad A;

XX DR WPI; 1998-348067/30.

XX PT New angiotensin II receptor binding compounds - useful for imaging  
XX cardiovascular diseases and disorders

XX PS Disclosure; Page 6; 99pp; English.

XX CC The invention relates to organic compounds of formula V-L-R; V = organic  
XX group having binding affinity for an angiotensin II receptor site; L = a  
XX linker group or a bond; R = a group detectable in vivo imaging of a  
XX human or animal body; provided that when V is angiotensin or a peptidic  
XX angiotensin derivative or analogue, then V-L-R is not a non-metal  
XX radionuclide substituted peptide and L-V is not simply a peptide with a  
XX chelating agent amide bonded to a side chain. Also claimed are: (1) 123I-  
XX losartan and 131I-losartan; (2) the use of the organic compound for the  
XX manufacture of a contrast medium for use in diagnosis involving  
XX administration of the contrast medium to an animate subject and  
XX generation of an image of at least part of the subject; (3) a method of  
XX generating an image of an animate subject comprising administration of a  
XX contrast agent comprising the organic compound and generating an image  
XX of at least part of the subject and (4) a method of monitoring the  
XX effect of treatment of animals with a drug to combat or provoke effects  
XX associated with angiotensin II comprising administration of the organic

CC compound and detecting the uptake of the agent by angiotensin II  
CC receptors, the administration and detection being optionally (and  
CC preferably) effected repeatedly. The organic compounds are useful for  
CC imaging cardiovascular diseases and disorders. The present sequence  
CC is shown in the specification.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYIHP 6

Db 1 rvyihp 6

RESULT 6

AAAY49590

ID AAY49590 standard; peptide; 6 AA.

XX

AC AAY49590;

XX 13-JAN-2000 (first entry)

DT

DE Angiotensin analogue peptide SEQ ID NO:5.

XX

KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;  
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.

XX

OS Synthetic.

XX

PN WO9952540-A1.

XX

PD 21-OCT-1999.

XX

PF 07-APR-1999; 99WO-US07654.

XX

PR 09-APR-1998; 98US-0081262.

XX

PR 12-JUN-1998; 98US-0089024.

XX

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

PA

XX Rodgers KE, Dizerega G;

XX

XX WPI; 1999-620285/53.

DR

XX Treating or preventing infections in mammals using peptides derived

PT from angiotensin or angiotensin receptor agonists

XX

PS Claim 2; Page 10; 91pp; English.

XX

CC The present invention describes a method for treating or preventing  
CC infections in mammals by administering peptides (A) that are fragments  
CC or analogues (or their fragments) of angiotensinogen, angiotensin I or  
CC II, or angiotensin II AT<sub>2</sub>-type receptor agonists. (A) contain at least  
CC 3 consecutive amino acids (aa) from the sequence (S1):

CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;  
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane  
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH<sub>2</sub>), Gly,  
CC Asp(NH<sub>2</sub>) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,  
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,  
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr

CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;  
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;  
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =

CC sequences having R4 as a terminal Tyr residue are excluded. The method  
CC is particularly used in cases of bacterial infection (e.g. septic shock,  
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and  
CC parasitic infections. AAY49586 to AAY49623 represent specifically

CC claimed examples of (A).

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYIHP 6

Db 1 rvyihp 6

RESULT 7

AAAY33905

ID AAY33905 standard; peptide; 6 AA.

XX

AC AAY33905;

XX

DT 29-NOV-1999 (first entry)

XX

DE Angiotensin II analogue AII(2-7).

XX

KW embryonic stem cell; ES; angiotensin; totipotent cell;  
KW gene therapy; replacement therapy; angiotensin II; AII;  
KW analogue.

XX

OS Homo sapiens.

XX

PN WO9942122-A1.

XX

PD 26-AUG-1999.

XX

PF 16-FEB-1999; 99WO-US03243.

XX

PR 19-FEB-1998; 98US-0075179.

XX

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

PA

XX Dizerega G, Rodgers KE;

XX

XX WPI; 1999-527419/44.

DR

PT Promoting embryonal cell proliferation, using angiotensinogen and  
PT angiotensin peptides, analogs or fragments

XX

PS Claim 2; Page 8; 76pp; English.

XX

CC This is the amino acid sequence of the Angiotensin II analogue,  
CC AII(2-7). The formation of Angiotensin II (AII) is initiated by the  
CC action of renin on the plasma substrate angiotensinogen.

CC This results in Angiotensin I (AI) which then converted to AII by the  
CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
CC residues from AI (AAY42372).

CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and  
CC analogs, Angiotensin II (AII), AII analogs, AII fragments, or AII  
CC AT<sub>2</sub> type 2 receptor agonists can rapidly provide a large population  
CC of ESCs (Embryonic Stem Cell) for use in replacement therapy.

CC Similarly, methods that increase in vivo proliferation of ESCs will  
CC enhance the utility of replacement therapy by rapidly increasing local  
CC concentration of the stem cells and their progeny at the site of  
CC therapy. The method also increases the potential utility of ESCs as

CC vehicles for gene therapy in certain disorders by more efficiently  
CC providing a large number of such cells for transfection, and also by  
CC providing a more efficient means to rapidly expand transduced ESCs.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYIHP 6

Db 1 rvyihp 6

Db 1 rvyihp 6  
|||||

RESULT 8  
AAV30543  
ID AAY30543 standard; peptide; 6 AA.

XX AAY30543;

XX 18-NOV-1999 (first entry)

XX Amino acid sequence of angiotensin II fragment AII2-7.

XX Angiotensin; analogue; tissue equivalent; cell proliferation.

XX Synthetic.

XX W09946285-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-US05261.

XX 11-MAR-1998; 98US-0077499.

XX 12-JUN-1998; 98US-0089064.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-551360/46.

XX An improved method for producing a tissue equivalent with angiotensin I and II derived active agents

XX Claim 2; Page 53; 83pp; English.

XX AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII fragments and AII analogues. The peptides are used in the method of the invention. The specification describes an improved method for producing a tissue equivalent. The method comprises contacting the tissue equivalent with angiotensin I and II derived active agents. The methods are used for production and culture of tissue equivalents (three-dimensional cell and tissue culture systems), chosen from skin, dermis, bone, bone marrow, pancreas, heart valve, vascular graft, cartilage, ligament, collagen lattice, liver and kidney tissue equivalents. The methods and tissue culture systems are used for the long-term proliferation of cells and tissues CC in an in vitro environment that more closely approximates that found CC in vivo.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|||||

Db 1 rvyihp 6

RESULT 9  
AAV30587  
ID AAY30587 standard; peptide; 6 AA.

XX AAY30587;

XX 18-NOV-1999 (first entry)

XX Amino acid sequence of an angiotensin II (AII) fragment AII2-7.

XX Angiotensin; analogue; radiation mitigation; tissue damage;  
KW radiation therapy; bone marrow transplantation;  
KW megakaryocyte production; platelet production; cancer therapy;  
KW gene therapy; hematopoietic disorder.

XX Synthetic.

XX W09945945-A1.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US05194.

XX 10-MAR-1998; 98US-0077382.

XX 09-APR-1998; 98US-0081262.

XX 30-APR-1998; 98US-0083670.

XX 19-JUN-1998; 98US-0090096.

XX 22-JUN-1998; 98US-0090216.

XX 11-SEP-1998; 98US-0099957.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX (RODG/) RODGERS K E.

XX (DIZE/) DIZEREKA G.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-551209/46.

XX Claim 2; Page 86; 116pp; English.

XX AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII fragments and AII analogues. The peptides are used in the method of the invention. The specification describes a method for mitigating radiation induced tissue damage, improving the effectiveness of radiation therapy, to support bone marrow transplantation, and promoting megakaryocyte production and platelet production. The method comprises administration of the present peptides. The methods can be used to mitigate radiation induced tissue damage, to improve the effectiveness of radiation therapy, to support bone marrow transplantation, and to promote megakaryocyte production and mobilization and platelet production. They are used particularly in cancer therapy. They can also be used to provide megakaryocytes as vehicles for gene therapy in hematopoietic disorders, by providing a more efficient means to rapidly expand transduced megakaryocytes.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|||||

Db 1 rvyihp 6

RESULT 10  
AAV32718  
ID AAY32718 standard; peptide; 6 AA.

XX AAY32718;

XX 09-NOV-1999 (first entry)

XX Angiotensin II analogue AII(2-7).

XX Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;

KW chemotaxis; growth factor; liver regeneration; cirrhosis;  
 KW hepatocarcinoma; hepatectomy; transplantation.

XX Synthetic.  
 OS Homo sapiens.

XX WO9939743-A2.

XX 12-AUG-1999.

XX 08-FEB-1999; 99WO-US02618.

XX 13-NOV-1998; 98US-0108412.

XX 09-FEB-1998; 98US-0074104.

XX (DIZE/) DIZEREGA G.

XX (RODG/) RODGERS K E.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1999-508461/42.

XX Hepatic cell proliferation with angiotensin I and II derived active

XX agents, useful for regeneration of liver after resection

XX Claim 2; Page 9; 66pp; English.

XX Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The  
 CC peptides are derived from the AII peptide (AAY32750). AII increases  
 CC mitogenesis and chemotaxis in cultured cells, and also increases the  
 CC release of growth factors and extracellular matrices. AII has also been  
 CC shown to increase the proliferation of certain cell types. The AII  
 CC analogue peptides can be used as the active agent in a method for  
 CC promoting hepatic cell proliferation and differentiation. The method  
 CC involves contacting the hepatic cells with an amount effective enough to  
 CC promote proliferation of any of the peptides. This method is useful in  
 CC liver regeneration following resection of hepatocarcinomas, hepatitis  
 CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic  
 CC failure, hepatocyte transplantation, liver transplantation and other  
 CC hepatic disorders where rapid regeneration of the liver is desirable. The  
 CC methods are also useful in rapidly providing a large population of  
 CC hepatic cells for use in cell therapy and for providing a large  
 CC population of transfected hepatic cells for use in gene therapy.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYVIHP 6

Db 1 rvyihp 6

RESULT 11

AAY33772

ID AAY33772 standard; peptide; 6 AA.

XX AAY33772;

XX 09-NOV-1999 (first entry)

XX Angiotensin II (AII) octapeptide fragment AII(2-7).

XX Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;  
 KW neuronal cell proliferation; differentiation; Alzheimer's disease;  
 KW Parkinson's disease; neuron replacement therapy.

XX Homo sapiens.

XX

PN WO9942123-A1.

XX 26-AUG-1999.

XX 19-FEB-1999; 99WO-US03772.

XX 19-FEB-1998; 98US-0075232.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1999-527420/44.

XX Promoting neuronal cell proliferation and differentiation

XX Claim 2; Page 10; 62pp; English.

XX Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin  
 CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The  
 CC application of angiotensin to wound tissue significantly increases the  
 CC rate of wound healing. AII is known to increase mitogenesis and  
 CC chemotaxis in cultured cells, and also increases their release of growth  
 CC factors and extracellular matrices, implicating it in cell growth and  
 CC differentiation. AT2 receptors are receptors for AII and are thought to  
 CC be involved in the mediation of the cell differentiation effects of AII.  
 CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal  
 CC cell proliferation or differentiation. This method is useful in the  
 CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement  
 CC therapy.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYVIHP 6

Db 1 rvyihp 6

RESULT 12

AAY15349

ID AAY15349 standard; peptide; 6 AA.

XX AAY15349;

XX 09-NOV-1999 (first entry)

XX Angiotensin II (AII) analogue, AII(2-7).

XX burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;  
 KW AII; analogue; chronic renal failure; cancer; bone marrow.

XX Synthetic.

XX Homo sapiens.

XX WO9940106-A2.

XX 12-AUG-1999.

XX 08-FEB-1999; 99WO-US02648.

XX 09-DEC-1998; 98US-0111535.

XX 09-FEB-1998; 98US-0074106.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1999-508486/42.

XX Promoting erythropoiesis with angiotensin I and II derived active  
 PT agents, useful for treatment of, e.g. congenital or acquired  
 PT aplastic or hypoplastic anemia  
 XX  
 PS Claim 2; Page 9; 76pp; English.  
 XX  
 CC This sequence is an angiotensin II (AII) analogue. Similar sequences  
 CC also based on the AII peptide have been tested against each other, AII  
 CC and a negative control. These active agents have been shown to affect  
 CC the levels of BFU-E (burst forming units-erythroid) in culture.  
 CC The active agents (AAV15348, AAV15359, AAV15372, AAV15379, and AAV15380)  
 CC augment erythropoiesis by potentiating erythropoietin-induced  
 CC differentiation. Increasing the rate of erythropoiesis improves clinical  
 CC benefits for the treatment of congenital or acquired aplastic or  
 CC hypoplastic anemia associated with chronic renal failure, end-stage renal  
 CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,  
 CC bone marrow transplantation and chronic diseases.  
 CC The active agents permit the use of smaller doses of erythropoietin  
 CC therefore decreasing treatment costs.  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIYHP 6  
 | | | | |  
 Db 1 rviyhp 6

## RESULT 13

AAV15309  
 ID AAV15309 standard; peptide; 6 AA.

XX  
 AC AAV15309;

XX  
 DT 09-NOV-1999 (first entry)

XX  
 DE Angiotensin II (AII) analogue, AII(2-7).

XX  
 KW angiotensin; angiotensin II; AII; wound healing; scarring;  
 KW tissue repair; agonist; analogue.

XX  
 OS Synthetic.

OS Homo sapiens.

XX  
 PN W09940107-A2.

XX  
 PD 12-AUG-1999.

XX  
 PF 08-FEB-1999; 99WO-US02725.

XX  
 PR 09-FEB-1998; 98US-0074105.

XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX  
 PI Dizerega G, Rodgers KE;

XX  
 DR WPI; 1999-508487/42.

XX  
 PT Epithelial stem cell and keratinocyte proliferation with angiotensin  
 PT I and II derived active agents, useful for treatment of skin wounds

XX  
 PS Claim 2; Page 10; 70pp; English.

XX  
 CC This is the amino acid sequence of an Angiotensin II analogue. This and  
 CC other similar analogues (AAV15306 to AAV15316 and AAV15321 to AAV15337)  
 CC can be used to promote the proliferation of epithelial stem cells and  
 CC keratinocytes leading to a more rapid and efficient cellular response to  
 CC stratified epithelial injury. The angiotensin analogues are derived from

CC an octapeptide present in humans and other species which has the  
 CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAV15342) and is known as  
 CC angiotensin II (AII). This is formed by the action of renin on the  
 CC plasma substrate angiotensinogen, the product of this reaction is a  
 CC decapeptide called angiotensin I (AI) which is converted to AII by the  
 CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
 CC residues from AI (AAV15339).  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIYHP 6  
 | | | | |  
 Db 1 rviyhp 6

## RESULT 14

AAV27405  
 ID AAV27405 standard; Peptide; 6 AA.

XX  
 AC AAV27405;

XX  
 DT 23-JAN-2001 (first entry)

XX  
 DE Angiotensin II analog AII(2-7).

XX  
 KW Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;  
 KW cardiomyopathies; inflammation; infection; sepsis; ischemia;  
 KW heart valve disease; myocarditis; angiotensin.

XX  
 OS Synthetic.

XX  
 PN W0200053211-A2.

XX  
 PD 14-SEP-2000.

XX  
 PF 09-MAR-2000; 2000WO-US06198.

XX  
 PR 09-MAR-1999; 99US-0123678.

XX  
 PR 31-AUG-1999; 99US-0151874.

XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX  
 PI Rodgers K, Dizerega G;

XX  
 DR WPI; 2000-611400/58.

XX  
 PT Promoting myocyte proliferation and myocardial tissue repair by  
 PT contacting myocytes with angiotensinogen or angiotensin I or II, useful  
 PT for treating heart attacks, cardiomyopathies, inflammation and  
 PT infection.

XX  
 PS Claim 2; Page 10; 55pp; English.

XX  
 CC The present invention relates to a method of promoting myocyte  
 CC proliferation or differentiation by contacting myocytes with an active  
 CC agent containing angiotensinogen, angiotensin I and II (AI, AII), and  
 CC angiotensin analogs. The present sequence is an angiotensin II analog  
 CC of the invention. The active agents of the invention may be useful for  
 CC promoting myocardial tissue repair following myocardial injury and for  
 CC treating heart failure in a mammal. Administration to accelerate in  
 CC vivo myocyte proliferation and/or to treat myocardial injuries can be  
 CC used to treat cardiomyopathies, inflammation, infection, sepsis,  
 CC ischemia, heart valve disease, myocarditis, inflammation, myocardial  
 CC ischemia and infarction and for improving cardiac output by increasing  
 CC stroke volume.

XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
|  
Db 1 rvyihp 6

## RESULT 15

AAB28103  
ID AAB28103 standard; Peptide; 6 AA.

XX AC AAB28103;  
XX

DT 26-JAN-2001 (first entry)

XX Angiotensin II analogue SEQ ID NO: 5.

DE Wound; scar formation; healing; adhesion formation; AII;  
KW angiotensin II analogue; scar treatment.  
XX

OS Synthetic.

XX WO200056345-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-0507669.

XX 23-MAR-1999; 99US-0125707.

XX 16-JUN-1999; 99US-0139541.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers K, Dizerega G;

XX WPI; 2000-587607/55.

XX Limiting scar or adhesion formation comprises administering at least  
PT one active agent comprising a peptide -

XX Claim 2; Page 10; 54pp; English.

XX The present invention is concerned with peptide analogues of angiotensin  
CC II (AII) which can be used to limit scar and adhesion formation. The  
CC application of AII to wound tissue results in a rapid increase in the  
CC rate of wound healing and causes the proliferation of certain cells, such  
CC as epithelial cells and keratinocytes. Analogues of the protein have been  
CC shown to reduce scar formation, and can be used not only to limit new  
CC scar formation but also to therapeutically treat existing scars. The  
CC wound types include lacerations, burns, punctures, trauma, ulcers, of  
CC periodontal conditions, laparotomy and incisional wounds, revision of  
CC hypertrophic scars, genetic hypertrophic scars, keloid scars,  
CC contractures after burns and cosmetic surgical procedures.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
|  
Db 1 rvyihp 6

Search completed: July 1, 2002, 07:41:55  
Job time: 347 sec

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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:00 ; Search time 59.1 Seconds  
(without alignments)  
2.480 Million cell updates/sec

Title: US-09-723-197-5  
Perfect score: 35  
Sequence: 1 RVYIHP 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pap: \*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pap: \*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	2	US-08-465-775-5
2	35	100.0	6	3	US-09-208-337-5
3	35	100.0	6	3	US-08-990-664-6
4	35	100.0	6	4	US-09-373-962-5
5	35	100.0	6	4	US-09-245-680-5
6	35	100.0	6	4	US-09-198-806C-5
7	35	100.0	6	4	US-09-352-191-5
8	35	100.0	6	4	US-09-012-400-5
9	35	100.0	7	1	US-08-021-839A-4
10	35	100.0	7	1	US-07-776-272-3
11	35	100.0	7	1	US-08-337-781-3
12	35	100.0	7	2	US-08-115-968-6
13	35	100.0	7	2	US-08-115-968-9
14	35	100.0	7	2	US-08-115-968-10
15	35	100.0	7	2	US-08-115-968-11
16	35	100.0	7	2	US-08-115-968-12
17	35	100.0	7	2	US-08-115-968-13
18	35	100.0	7	2	US-08-115-968-14
19	35	100.0	7	2	US-08-115-968-15
20	35	100.0	7	2	US-08-115-968-16
21	35	100.0	7	2	US-08-360-784B-3
22	35	100.0	7	2	US-08-465-775-2
23	35	100.0	7	2	US-08-465-775-4
24	35	100.0	7	3	US-09-054-308A-3
25	35	100.0	7	3	US-09-208-337-2
26	35	100.0	7	3	US-09-208-337-4
27	35	100.0	7	3	US-08-990-664-3

28	35	100.0	7	3	US-08-990-664-5	Sequence 5, Appli
29	35	100.0	7	3	US-08-990-664-38	Sequence 38, Appl
30	35	100.0	7	3	US-08-990-664-46	Sequence 46, Appl
31	35	100.0	7	4	US-09-210-249-2	Sequence 2, Appli
32	35	100.0	7	4	US-09-373-962-2	Sequence 2, Appli
33	35	100.0	7	4	US-09-373-962-4	Sequence 4, Appli
34	35	100.0	7	4	US-09-245-680-2	Sequence 2, Appli
35	35	100.0	7	4	US-09-245-680-4	Sequence 4, Appli
36	35	100.0	7	4	US-09-198-806C-2	Sequence 2, Appli
37	35	100.0	7	4	US-09-198-806C-4	Sequence 4, Appli
38	35	100.0	7	4	US-09-352-191-2	Sequence 2, Appli
39	35	100.0	7	4	US-09-352-191-4	Sequence 4, Appli
40	35	100.0	7	4	US-09-012-400-2	Sequence 2, Appli
41	35	100.0	7	4	US-09-012-400-4	Sequence 4, Appli
42	35	100.0	7	5	PCT-US94-10258-6	Sequence 6, Appli
43	35	100.0	7	5	PCT-US94-10258-9	Sequence 9, Appli
44	35	100.0	7	5	PCT-US94-10258-10	Sequence 10, Appl
45	35	100.0	7	5	PCT-US94-10258-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-08-465-775-5  
; Sequence 5, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-775-5

Query Match 100.0%; Score 35; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RVYIHP 6  
Db 1 RVYIHP 6

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RESULT 2
US-09-208-337-5
; Sequence 5, Application US/09208337
; Patent No. 6096709
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gere, dizerega
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/208,337
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,775
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/337,781
; FILING DATE: 14-NOV-1994
; APPLICATION NUMBER: 08/126,368
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC010.001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 949-760-0404
; TELEFAX: 949-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-208-337-5

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIHP 6
Db 1 RVIHP 6

RESULT 3
US-09-990-664-6
; Sequence 6, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; TITLE OF INVENTION: IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
```

```
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA: US/08/990,664
APPLICATION NUMBER: US/08/990,664
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,310
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: USC012.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-990-664-6

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIHP 6
Db 1 RVIHP 6

RESULT 4
US-09-373-962-5
; Sequence 5, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
; FILE REFERENCE: 98364A
; CURRENT APPLICATION NUMBER: US/09/373,962
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)
US-09-373-962-5

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIHP 6
Db 1 RVIHP 6
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RESULT 5  
US-09-245-680-5  
; Sequence 5, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245,680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)  
US-09-245-680-5

Query Match 100.0%; Score 35; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 1 RVIHP 6

RESULT 6  
US-09-198-806C-5  
; Sequence 5, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: Method and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)  
US-09-198-806C-5

Query Match 100.0%; Score 35; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 1 RVIHP 6

RESULT 7  
US-09-352-191-5  
; Sequence 5, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue

; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352,191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)  
US-09-352-191-5

Query Match 100.0%; Score 35; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 1 RVIHP 6

RESULT 8  
US-09-012-400-5  
; Sequence 5, Application US/09012400D  
; Patent No. 6335195  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell  
; TITLE OF INVENTION: Proliferation and Differentiation  
; FILE REFERENCE: 97,017-G  
; CURRENT APPLICATION NUMBER: US/09/012,400D  
; CURRENT FILING DATE: 1998-01-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (2-7)  
US-09-012-400-5

Query Match 100.0%; Score 35; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 1 RVIHP 6

RESULT 9  
US-08-021-839A-4  
; Sequence 4, Application US/08021839A  
; Patent No. 5326776  
; GENERAL INFORMATION:  
; APPLICANT: Winn, Martin  
; APPLICANT: De, Biswanath  
; APPLICANT: Zydowsky, Thomas M.  
; APPLICANT: Kerkman, Daniel J.  
; APPLICANT: DeBernardis, John F.  
; APPLICANT: Rosenberg, Saul H.  
; APPLICANT: Shiosaki, Kazumi  
; APPLICANT: Basha, Fatima Z.  
; APPLICANT: Spina, Kenneth P.  
; APPLICANT: Von Geldern, Thomas W.  
; TITLE OF INVENTION: Angiotensin II Receptor Antagonists  
; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edward H. Gorman, Jr.  
; STREET: Abbott Laboratories  
; STREET: D-377/AP6D  
; STREET: One Abbott Park Road  
; CITY: Abbott Park  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb  
; COMPUTER: Apple Macintosh Iicx  
; OPERATING SYSTEM: Macintosh  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/021,839A  
; FILING DATE: 24-FEB-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/844,817  
; FILING DATE: 02-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steven R. Crowley  
; REGISTRATION NUMBER: 31,604  
; REFERENCE/DOCKET NUMBER: 5136, US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708) 938-7742  
; TELEFAX: (708) 938-2623  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acid residues  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; DESCRIPTION: peptide  
; US-08-021-839A-4

Query Match 100.0%; Score 35; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIHP 6  
Db 1 RVIHP 6

RESULT 10  
US-07-776-272-3  
; Sequence 3, Application US/07776272  
; Patent No. 5612454  
; GENERAL INFORMATION:  
; APPLICANT: Kaminuma, Toshihiko  
; APPLICANT: Iida, Toshi  
; APPLICANT: Tajima, Masahiro  
; TITLE OF INVENTION: Process for Purification of Polypeptide  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wegner, Cantor, Mueller & Player  
; STREET: 1233 20th St. N.W. P.O. Box 18218  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: United States of America  
; ZIP: 20036-8218  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/776,272  
; FILING DATE: 19911129  
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: P-450-23167  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-0400  
; TELEFAX: 202-887-0605  
; TELEX: 440706  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: YES  
; US-07-776-272-3

Query Match 100.0%; Score 35; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIHP 6  
Db 1 RVIHP 6

RESULT 11  
US-08-337-781-3  
; Sequence 3, Application US/08337781  
; Patent No. 5629292  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: diZerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS  
; TITLE OF INVENTION: THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Robbins, Berliner & Carson  
; STREET: 201 No. 5629292th Figueroa Street, Fifth Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/337,781  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-336C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-337-781-3

Query Match 100.0%; Score 35; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
|||||  
Db 1 RVIHP 6

RESULT 12  
US-08-115-968-6  
; Sequence 6, Application US/08115968  
; Patent No. 5824696  
; GENERAL INFORMATION:  
; APPLICANT: Griswold E, Don  
; APPLICANT: Wharton, John  
; TITLE OF INVENTION: Medicaments  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham  
; STREET: P. O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/115,968  
; FILING DATE: 01-SEP-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dinner, Dara L  
; REGISTRATION NUMBER: 33,680  
; REFERENCE/DOCKET NUMBER: P50192  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 270-5017  
; TELEFAX: (610) 270-5090  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Inhibitory-site  
; LOCATION: 1..2  
; OTHER INFORMATION: /product= "other"  
; OTHER INFORMATION: /note= "hydroxyacetal of Arg"  
; FEATURE:  
; NAME/KEY: Inhibitory-site  
; LOCATION: 6..7  
; OTHER INFORMATION: /product= "other"  
; OTHER INFORMATION: /note= "methyl ester of Thr"  
US-08-115-968-6

Query Match 100.0%; Score 35; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
|||||  
Db 1 RVIHP 6

RESULT 13  
US-08-115-968-9  
; Sequence 9, Application US/08115968  
; Patent No. 5824696  
; GENERAL INFORMATION:  
; APPLICANT: Griswold E, Don  
; APPLICANT: Wharton, John

; TITLE OF INVENTION: Medicaments  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham  
; STREET: P. O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/115,968  
; FILING DATE: 01-SEP-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dinner, Dara L  
; REGISTRATION NUMBER: 33,680  
; REFERENCE/DOCKET NUMBER: P50192  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 270-5017  
; TELEFAX: (610) 270-5090  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Inhibitory-site  
; LOCATION: 1..2  
; OTHER INFORMATION: /product= "other"  
; OTHER INFORMATION: /note= "aminocycetyl deriv of arg"  
US-08-115-968-9

Query Match 100.0%; Score 35; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
|||||  
Db 1 RVIHP 6

RESULT 14  
US-08-115-968-10  
; Sequence 10, Application US/08115968  
; Patent No. 5824696  
; GENERAL INFORMATION:  
; APPLICANT: Griswold E, Don  
; APPLICANT: Wharton, John  
; TITLE OF INVENTION: Medicaments  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham  
; STREET: P. O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/115,968  
; FILING DATE: 01-SEP-1993

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dinner, Dara L  
REGISTRATION NUMBER: 33,680  
REFERENCE/DOCKET NUMBER: P50192  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5017  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Inhibitory-site  
LOCATION: 1..2  
OTHER INFORMATION: /product= "other"  
OTHER INFORMATION: /note= "aminooxypropionyl deriv of arg"  
US-08-115-968-10

Query Match 100.0%; Score 35; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYIHP 6  
Db 1 RYIHP 6

RESULT 15  
US-08-115-968-11  
Sequence 11, Application US/08115968  
Patent No. 5824696  
GENERAL INFORMATION:  
APPLICANT: Griswold E, Don  
APPLICANT: Wharton, John  
TITLE OF INVENTION: Medicaments  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham  
STREET: P. O. Box 1539  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/115,968  
FILING DATE: 01-SEP-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dinner, Dara L  
REGISTRATION NUMBER: 33,680  
REFERENCE/DOCKET NUMBER: P50192  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5017  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Inhibitory-site

LOCATION: 1..2  
OTHER INFORMATION: /product= "other"  
OTHER INFORMATION: /note= "hydroxyacetal deriv of arg"  
US-08-115-968-11

Query Match 100.0%; Score 35; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYIHP 6  
Db 1 RYIHP 6

Search completed: July 1, 2002, 07:43:00  
Job time: 301 sec

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**THIS PAGE BLANK (USF70)**

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:27 ; Search time 69.93 Seconds  
(without alignments)  
8.244 Million cell updates/sec

Title: US-09-723-197-5  
Perfect score: 35  
Sequence: 1 RVIHP 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	100.0	10	2	S65432	angiotensin I - ho
2	35	100.0	14	2	A01250	angiotensin precu
3	35	100.0	15	2	A60834	angiotensin I prec
4	35	100.0	476	1	JC2318	angiotensin precu
5	35	100.0	477	1	ANRT	angiotensin precu
6	35	100.0	477	1	A29978	angiotensin precu
7	35	100.0	485	1	ANHU	angiotensin precu
8	35	100.0	540	2	S72233	transcription fact
9	34	97.1	10	2	A60624	angiotensin I - Ja
10	34	97.1	10	2	A90917	angiotensin precu
11	34	97.1	10	2	A90345	angiotensin precu
12	34	97.1	316	2	T34838	probable transfera
13	33	94.3	11	2	S07207	Criinia-angiotensin
14	32	91.4	177	2	C71329	hypothetical prote
15	32	91.4	444	2	T20803	hypothetical prote
16	32	91.4	681	2	I78558	hypothetical brach
17	32	91.4	695	2	T24950	hypothetical prote
18	32	91.4	701	1	S46458	transcription fact
19	32	91.4	702	2	G01840	T-box protein 2 -
20	32	91.4	974	1	A40213	optic lobe develop
21	31	88.6	173	2	S72230	transcription fact
22	31	88.6	184	2	S72231	transcription fact
23	31	88.6	274	2	B90430	hypothetical prote
24	31	88.6	288	2	T48753	conserved hypothet
25	31	88.6	300	2	S24057	ferritin 2 precurs
26	31	88.6	370	2	AC0173	probable iron-sulf
27	31	88.6	482	1	VHVUCH	nucleocapsid prote
28	31	88.6	485	1	VHVUJ	nucleoprotein - Ha
29	31	88.6	539	2	T46720	hypothetical prote

conserved hypothet  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
probable serine/th  
mutator protein mu  
hypothetical prote  
conserved hypothet  
hypothetical prote  
hypothetical prote  
probable ATP-depen  
probable GDP-manno  
adhalin - mouse  
adhalin - golden h  
hypothetical prote  
gastrulation regul

ALIGNMENTS

RESULT 1

S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432  
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen  
Eur. J. Biochem. 237, 414-423, 1996

A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipt  
A:Reference number: S65431; MUID:96215437  
A:Accession: S65432  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <WIJ>  
A>Note: the source is designated as Haematobia irritans exigu

Query Match 100.0%; Score 35; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
| | | | |  
Db 2 RVIHP 7

RESULT 2

A01250  
angiotensin precursor - horse (fragment)  
C:Species: Equus caballus (domestic horse)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998  
C:Accession: A92775; A01250  
R:Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957

A:Reference number: A92775  
A:Accession: A92775  
A:Molecule type: protein  
A:Residues: 1-14 <SKE>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F;1-10/Product: angiotensin I #status experimental <AN1>  
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 35; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
| | | | |  
Db 2 RVIHP 7

## RESULT 3

A60834  
angiotensin I precursor - dog (fragment)  
N:Alternate names: angiotensinogen I  
N:Contains: angiotensin I  
C:Species: Canis lupus familiaris (dog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1998  
C:Accession: A60834  
R:Oliver, J.A.

Hypertension 11, 21-27, 1988  
A:Title: Purification and partial characterization of canine angiotensinogen.  
A:Reference number: A60834; MUID:88113996

A:Accession: A60834  
A:Molecule type: protein  
C:Residues: 1-15 <OLJ>  
C:Superfamily: antithrombin III  
C:Keywords: glycoprotein; plasma  
F:1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 35; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYIHP 6

|||||

Db 2 RYIHP 7

## RESULT 4

JC2318  
angiotensin precursor - sheep  
N:Alternate names: angiotensinogen  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: JC2318; A25406  
R:Nagase, M.; Suzuki, F.; Fukumizu, A.; Takeda, N.; Murakami, K.; Nakamura  
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994  
A:Title: Sequencing and expression of sheep angiotensinogen cDNA.  
A:Reference number: JC2318; MUID:95072318

A:Accession: JC2318

A:Molecule type: mRNA

A:Residues: 1-476 &lt;NAG&gt;

A:Cross-references: DBJ:DJ17520; NID:9575593; PIDN:BAA04470.1; PID:gl197183

A:Experimental source: liver

A&gt;Note: the authors translated the codon TTC for residue 465 as Leu

R:Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.

Eur. J. Biochem. 154, 597-601, 1986

A:Title: Purification and characterization of ovine angiotensinogen.

A:Reference number: A25406; MUID:86136099

A:Accession: A25406

A:Molecule type: protein

A:Residues: 25-37, X', 39 &lt;FER&gt;

C:Superfamily: antithrombin III

C:Keywords: blood pressure control; glycoprotein

F:1-24/Domain: signal sequence #status predicted &lt;STG&gt;

F:24-476/Product: angiotensinogen #status predicted &lt;MPT&gt;

F:25-34/Product: angiotensin #status predicted &lt;MAT&gt;

F:295,362/Binding site: carboxylate (Asn) (covalent) #status predicted

## Query Match

100.0%; Score 35; DB 1; Length 476;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYIHP 6

|||||

Db 26 RYIHP 31

## RESULT 5

ANRT

angiotensin precursor - rat  
N:Contains: angiotensin I; angiotensin II; angiotensin III  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 18-Jun-1999  
C:Accession: A93945; A90456; A01251  
R:Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983  
A:Title: Cloning and sequence analysis of cDNA for rat angiotensinogen.  
A:Reference number: A93945; MUID:83169849  
A:Accession: A93945

A:Molecule type: mRNA

A:Residues: 1-477 &lt;OHK&gt;

A:Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914

R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.

Biochemistry 20, 7010-7015, 1981

A:Title: Rat angiotensinogen and Des(antiotensin I)angiotensinogen: purification, char

A:Reference number: A90456; MUID:82091819

A:Accession: A90456

A:Molecule type: protein

A:Residues: 25-41 &lt;BOU&gt;

C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted

e I (angiotensin-converting enzyme), primarily in the lungs.

C:Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and

sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.

C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.

unq.

C:Superfamily: antithrombin III

C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

F:1-24/Domain: signal sequence #status predicted &lt;SIG&gt;

F:25-477/Product: angiotensinogen #status predicted &lt;MPT&gt;

F:25-34/Product: angiotensin I #status experimental &lt;PP1&gt;

F:25-32/Product: angiotensin II #status experimental &lt;PP2&gt;

F:26-32/Product: angiotensin III #status experimental &lt;PP3&gt;

F:295,319/Binding site: carboxylate (Asn) (covalent) #status predicted

## Query Match

100.0%; Score 35; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYIHP 6

|||||

Db 26 RYIHP 31

## RESULT 6

Az9978  
angiotensin precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A29978  
R:Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.

Genomics 2, 240-248, 1988

A:Title: Molecular cloning of the mouse angiotensinogen gene.

A:Reference number: A29978; MUID:88284703

A:Accession: A29978

A&gt;Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-477 &lt;CLO&gt;

A:Cross-references: GB:AF045887; GB:J03046; NID:g2842773; PIDN:AAC01765.1; PID:g28427

C:Genetics:

A:Introns: 277/1; 366/2; 414/3

C:Superfamily: antithrombin III

C:Keywords: blood pressure control

F:1-24/Domain: signal sequence #status predicted &lt;SIG&gt;

F:25-477/Product: angiotensinogen #status predicted &lt;MAT&gt;

## Query Match

100.0%; Score 35; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYIHP 6



Db 26 RVIHP 31  
|||||

## RESULT 7

ANHU

angiotensin precursor [validated] - human  
N:Alternate names: angiotensinogen  
N:Contains: angiotensin I; angiotensin II; angiotensin III  
C:Species: Homo sapiens (man)  
C:Date: 06-Jul-1982 #sequence\_revision 19-Jan-1996 #text\_change 08-Dec-2000  
C:Accession: A35203; A31362; I37169; A60825; I39462; A90487; A90226; I54281; A01  
R:Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami,  
J. Biol. Chem. 265, 7576-7582, 1990  
A:Title: Structure and expression of the human angiotensinogen gene. Identification of a  
A:Reference number: A35203; MUID:90237063  
A:Accession: A35203  
A:Molecule type: DNA  
A:Residues: 1-485 <FKU>  
A:Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327  
R:Gaillard, I.; Clauser, E.; Corvol, P.  
DNA 8, 87-99, 1989  
A:Title: Structure of human angiotensinogen gene.  
A:Reference number: A31362; MUID:89170129  
A:Accession: A31362  
A:Molecule type: DNA  
A:Residues: 1-267, 'M', 269-332, 'E', 334-485 <GAI>  
A:Cross-references: GB:M24686; GB:M24687; GB:M24688  
A:Note: the authors translated the codon GAA for residue 333 as Gln  
R:Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.  
J. Biol. Chem. 269, 28598-28605, 1994  
A:Title: Identification of cell type-dependent enhancer core element located in the 3'-  
A:Reference number: I37168; MUID:95050659  
A:Accession: I37168  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-285 <NIB1>  
A:Cross-references: EMBL:X15324; NID:g1197496; PIDN:CAA33385.1; PID:g1197497  
A:Accession: I37169  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 287-375 <NIB2>  
A:Cross-references: EMBL:X15325; NID:Q28695  
R:Kunapuli, S.P.; Benedict, C.R.; Kumar, A.  
Arch. Biochem. Biophys. 254, 642-646, 1987  
A:Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.  
A:Reference number: A60825; MUID:87212053  
A:Accession: A60825  
A:Molecule type: mRNA  
A:Residues: 32-184 <KUN1>  
R:Kunapuli, S.P.; Kumar, A.  
Circ. Res. 60, 786-790, 1987  
A:Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence of  
A:Reference number: I39462; MUID:87244745  
A:Accession: I39462  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-267, 'M', 269-338 <KUN2>  
A:Cross-references: GB:M69110; NID:g178643; PIDN:AAA52282.1; PID:g553181  
R:Kageyama, R.; Ohkubo, H.; Nakanishi, S.  
Biochemistry 23, 3603-3609, 1984  
A:Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequ  
A:Reference number: A90487; MUID:85000455  
A:Accession: A90487  
A:Molecule type: mRNA  
A:Residues: 1-267, 'M', 269-485 <KAG>  
A:Cross-references: GB:K02215; NID:g178639; PIDN:AAA51731.1; PID:g178640  
A:Note: it is uncertain whether Met-1 or Met-10 is the initiator  
R:Tecksbury, D.A.; Dart, R.A.; Travis, J.  
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981  
A:Title: The amino terminal amino acid sequence of human angiotensinogen.  
A:Reference number: A90226; MUID:81255848  
A:Accession: A90226

A:Molecule type: protein  
A:Residues: 34-46, 'X', 48-50, 'S', 52-57, 'D' <TEW>  
R:Hixson, J.E.; Powers, P.K.  
Hum. Genet. 96, 110-112, 1995  
A:Title: Detection and characterization of new mutations in the human angiotensinogen  
A:Reference number: I54281; MUID:95331754  
A:Accession: I54281  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 176-241, 'I', 243-267, 'M', 269-287, 'ANLSAG' <HIX>  
A:Cross-references: GB:S78529; NID:g9993316; PIDN:AA014287.1; PID:g4261987  
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted  
e I (angiotensin-converting enzyme), primarily in the lungs.  
C:Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and  
sp-1) angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.  
C:Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels,  
o induces thirst.  
C:Comment: Angiotensin II and angiotensin III are equally potent in stimulating the s  
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.  
C:Genetics:  
A:Gene: GDB:AGT  
A:Cross-references: GDB:118750; OMIM:106150  
A:Map position: Iq42-Iq43  
A:Introns: 286/1; 375/2; 423/3  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor  
P:1-33/Domain: (or 10-33) signal sequence #status predicted <SIG>  
P:34-48/Product: angiotensinogen #status predicted <MP1>  
P:34-43/Product: angiotensin I #status experimental <PP1>  
P:34-41/Product: angiotensin II #status experimental <PP2>  
P:35-41/Product: angiotensin III #status experimental <PP3>  
P:47,170,304,328/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 35; DB 1; Length 485;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RVIHP 6  
Db 35 RVIHP 40  
RESULT 8  
S72233  
transcription factor tbx6 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C:Accession: S72233; S72232  
R:Agulnik, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: S72233  
A:Accession: S72233  
A:Molecule type: mRNA  
A:Residues: 1-540 <AGU>  
A:Cross-references: EMBL:U57331; NID:g1620601; PIDN:AA053110.1; PID:g1620602  
R:Agulnik, S.I.; Garvey, N.; Hancock, S.; Ruvinik, I.; Chapman, D.L.; Agulnik, I.; B  
Genetics 144, 249-254, 1996  
A:Title: Evolution of mouse T-box genes by tandem duplication and cluster dispersion.  
A:Reference number: S72230; MUID:97032942  
A:Accession: S72232  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 100-280 <AGW>  
A:Cross-references: EMBL:U57331  
C:Genetics:  
A:Gene: tbx6  
C:Superfamily: T-box homology  
C:Keywords: DNA binding  
P:100-282/Domain: T-box homology <TBX>  
Query Match 100.0%; Score 35; DB 2; Length 540;

Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|||||

Db 171 RVIYHP 176

RESULT 9  
A60624  
angiotensin I - Japanese quail  
C:Species: Coturnix coturnix japonica (Japanese quail)  
C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-May-1999  
C:Accession: A60624  
R:Takel, Y.; Hasegawa, Y.  
Gen. Comp. Endocrinol. 79, 12-22, 1990  
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of these effects by angiotensin II  
A:Reference number: A60624; MUID:90284684  
A:Accession: A60624  
A:Molecule type: protein  
A:Residues: 1-10 <NAK>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 97.1%; Score 34; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.26;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|||||

Db 2 RVIYHP 7

RESULT 10  
A90917  
angiotensin precursor - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A90917; A01250  
R:Nakayama, T.; Nakajima, T.; Sokabe, H.  
Chem. Pharm. Bull. 21, 2085-2087, 1973  
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its precursor  
A:Reference number: A90917; MUID:74127845  
A:Accession: A90917  
A:Molecule type: protein  
A:Residues: 1-10 <NAK>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 34; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.26;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|||||

Db 2 RVIYHP 7

RESULT 11  
A90345  
angiotensin precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A90345; A01250  
R:Elliot, D.F.; Peart, W.S.  
Biochem. J. 65, 246-254, 1957  
A:Title: The amino acid sequence in a hypertensin.  
A:Reference number: A90345  
A:Accession: A90345  
A:Molecule type: protein

A:Residues: 1-10 <ELL>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 34; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.26;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|||||

Db 2 RVIYHP 7

RESULT 12  
T34838  
probable transferase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
C:Accession: T34838  
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
Submitted to the EMBL Data Library, February 1999  
A:Reference number: Z21559  
A:Accession: T34838  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-316 <OLI>  
A:Cross-references: EMBL:AL035478; PIDN:CA36592.1; GSPDB:GN00070; SCOEDB:SC2G5.05  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC2G5.05

Query Match 97.1%; Score 34; DB 2; Length 316;  
Best Local Similarity 83.3%; Pred. No. 12;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|||||

Db 218 RVIYHP 223

RESULT 13  
S07207  
Crinia-angiotensin, skin - frog (Crinia georgiana)  
C:Species: Crinia georgiana  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Aug-2000  
C:Accession: S07207  
R:Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.  
Experientia 35, 1132-1133, 1979  
A:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II precursor  
A:Reference number: S07207; MUID:80024575  
A:Accession: S07207  
A:Molecule type: protein  
A:Residues: 1-11 <ERS>  
C:Superfamily: unassigned animal peptides

Query Match 94.3%; Score 33; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 0.48;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
|:|:|

Db 5 RVIYHP 10

RESULT 14  
C71329  
hypothetical protein TP0404 - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 05-Nov-1999

C:Accession: C71329  
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDevitt, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770  
A:Accession: C71329  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-177 <COL>  
A:Cross-references: GB:AF001218; GB:AF000520; NID:G3322678; PIDN:AAC65395.1; PID:G332269  
A:Experimental source: strain Nichols  
C:Genetics:  
A:Gene: TP0404

Query Match 91.4%; Score 32; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIYHP 6  
:|||||  
Db 2 KVIYHP 7

RESULT 15  
T20803  
hypothetical protein F12F6.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T20803  
R:Kershaw, J.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19326  
A:Accession: T20803  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-444 <WIL>  
A:Cross-references: EMBL:Z73425; PIDN:CAA97789.1; GSPDB:GN00022; CESP:F12F6.3  
A:Experimental source: clone F12F6  
C:Genetics:  
A:Gene: CESP:F12F6.3  
A:Map position: 4  
A:Introns: 27/2; 75/2; 101/2; 161/3; 188/3; 243/3; 284/2; 388/3; 428/3

Query Match 91.4%; Score 32; DB 2; Length 444;  
Best Local Similarity 83.3%; Pred. No. 47;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIYHP 6  
:|||||  
Db 46 KVIYHP 51

Search completed: July 1, 2002, 07:45:28  
Job time: 449 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:07 ; Search time 34.05 Seconds  
(without alignments)  
6.823 Million cell updates/sec

Title: US-09-723-197-5  
Perfect score: 35  
Sequence: 1 RVIHP 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	35	100.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
2	35	100.0	14	1 ANG1_HORSE	P01016 equus cabal
3	35	100.0	436	1 TBX6_HUMAN	O95947 homo sapien
4	35	100.0	476	1 ANG1_SHEEP	P20757 ovis aries
5	35	100.0	477	1 ANG1_MOUSE	P11859 mus musculu
6	35	100.0	477	1 ANG1_RAT	P01015 rattus norv
7	35	100.0	485	1 ANG1_HUMAN	P01019 homo sapien
8	35	100.0	501	1 TX18_HUMAN	O95935 homo sapien
9	35	100.0	540	1 TBX6_MOUSE	P70327 mus musculu
10	35	100.0	602	1 TX15_MOUSE	O70306 mus musculu
11	35	100.0	613	1 TX18_MOUSE	O96926 mus musculu
12	34	97.1	10	1 ANG1_BOTJA	Q10581 bothrops ja
13	34	97.1	10	1 ANG1_BOVIN	P01017 bos taurus
14	34	97.1	10	1 ANG1_CHICK	P01018 gallus gall
15	33	94.3	11	1 ANG1_CRIGE	P09037 crinia geor
16	32	91.4	177	1 Y404_TREPA	O83419 treponema p
17	32	91.4	378	1 EXT1_CAEEL	O01704 caenorhabdi
18	32	91.4	414	1 TBX3_CHICK	O73718 gallus gall
19	32	91.4	681	1 TBX1_MOUSE	Q64336 mus musculu
20	32	91.4	682	1 TBX1_HUMAN	Q16650 homo sapien
21	32	91.4	701	1 TBX2_MOUSE	Q60707 mus musculu
22	32	91.4	702	1 TBX2_HUMAN	Q15219 homo sapien
23	32	91.4	742	1 TBX3_HUMAN	O15119 homo sapien
24	32	91.4	988	1 OMB1_DROME	Q24432 drosophila
25	31	88.6	173	1 TBX4_MOUSE	P70325 mus musculu
26	31	88.6	251	1 TX20_HUMAN	Q9umr3 homo sapien
27	31	88.6	297	1 TX20_MOUSE	Q9es03 mus musculu
28	31	88.6	300	1 FR12_MAIZE	P29390 zea mays (m
29	31	88.6	482	1 NCAP_CCFEV	P27317 crimean-con
30	31	88.6	485	1 NCAP_HAZVJ	P27318 hazara viru
31	31	88.6	518	1 TBX5_HUMAN	Q99593 homo sapien
32	31	88.6	518	1 TBX5_MOUSE	P70326 mus musculu
33	31	88.6	535	1 TX21_HUMAN	Q9u117 homo sapien

34	31	88.6	545	1 TBX4_HUMAN	P57082 homo sapien
35	31	88.6	617	1 THRB_RAT	P18292 rattus norv
36	31	88.6	622	1 THRB_HUMAN	P00734 homo sapien
37	31	88.6	625	1 THRB_BOVIN	P00735 bos taurus
38	31	88.6	646	1 KBDE_SCHPO	Q10364 schizosacch
39	31	88.6	692	1 EOMD_XENLA	P79944 xenopus lae
40	31	88.6	981	1 EPA3_BRARE	O13146 brachydanio
41	30	85.7	169	1 ADPP_METJA	Q58549 methanococc
42	30	85.7	361	1 TBXL_CHICK	P79779 gallus gall
43	30	85.7	387	1 SCA_MESAU	O64255 mesocricetu
44	30	85.7	387	1 SCA_MOUSE	P82350 mus musculu
45	30	85.7	397	1 TBXT_CHICK	P79778 gallus gall

ALIGNMENTS

```
RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;
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Query Match 100.0%; Score 35; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RVIHP 6  
DB 2 RVIHP 7

```
RESULT 2
ANG1_HORSE
ID ANG1_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN SERPIN8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
RT polypeptide renin substrate.";
```

RL J. Exp. Med. 106:439-453(1957).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR PIR: A01250; A01250. Serpin.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFDD7 CRC64;  
  
Query Match 100.0%; Score 35; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RVIYHP 6  
| | | | |  
Db 2 RVIYHP 7

RESULT 3  
TBX6\_HUMAN  
ID TBX6\_HUMAN STANDARD; PRT; 436 AA.  
AC O95947;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX6 (T-box protein 6).  
GN TBX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99134303; PubMed=99333572;  
RA Papapetrou C., Putt W., Fox M., Edwards Y.H.;  
RT "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";  
RL Genomics 55:238-241(1999).  
RN [2]  
RP SEQUENCE OF 135-272 FROM N.A.  
RC TISSUE=Myeloid;  
RX MEDLINE=99107806; PubMed=9888994;  
RA Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,  
RA Anstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;  
RT "Identification, mapping and phylogenomic analysis of four new human  
RT members of the T-box gene family: BOMES, TBX6, TBX18, and TBX19.";  
RL Genomics 55:10-20(1999).  
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN  
CC DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF  
CC PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).  
CC -1- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).  
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL  
CC TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT  
CC TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A  
CC SECOND PHASE IN SOME ADULT TISSUES.  
CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

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CC -----  
DR EMBL: AJ007989; CAA07812.1; -;  
DR EMBL: AJ010279; CAB37938.1; -;  
DR HSSP: P24781; 1XBR.  
DR MIM: 602427; -;  
DR InterPro: IPR001699; T-box.  
DR Pfam: PF00907; T-box; 1.  
DR PRINTS: PR00937; TBOX.  
DR SMART: SM00425; TBOX; 1.  
DR PROSITE: PS01283; TBOX\_1; 1.  
DR PROSITE: PS01264; TBOX\_2; 1.  
DR PROSITE: PS0252; TBOX\_3; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein;  
KW Developmental protein.  
FT DNA\_BIND 100 273 T-BOX.  
FT CONFLICT 207 207 H -> HV (IN REF. 2).  
SQ SEQUENCE 436 AA; 47017 MW; 438178BD31B966E9 CRC64;  
  
Query Match 100.0%; Score 35; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RVIYHP 6  
| | | | |  
Db 171 RVIYHP 176

RESULT 4  
ANGT\_SHEEP  
ID ANGT\_SHEEP STANDARD; PRT; 476 AA.  
AC P20757;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPINB8 OR AGT.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95072318; PubMed=7765514;  
RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,  
RA Murakami K., Nakamura Y.;  
RT "Sequencing and expression of sheep angiotensinogen cDNA.";  
RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).  
RN [2]  
RP SEQUENCE OF 25-39.  
RX MEDLINE=86136039; PubMed=3081342;  
RA Fernley R.T., John M., Niall H.D., Coghlan J.P.;  
RT "Purification and characterization of ovine angiotensinogen.";  
RL Eur. J. Biochem. 154:597-601(1986).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
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CC -----
CC DR EMBL: D17520; BAA04470.1; -.
CC DR PIR: A25406; A25406.
CC DR InterPro; IPR000217; Angiotensngn.
CC DR pfam; PF00079; serpin; 1.
CC DR PRINTS; PR00054; ANGIOTENSNGN.
CC DR SMART; SM00093; SERPIN; 1.
CC DR PROSITE; PS00284; SERPIN; 1.
CC DR VASOCONSTRICTOR; GLYCOPROTEIN; Plasma; Serpin; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 476 ANGIOTENSINOGEN.
CC FT PEPTIDE 25 34 ANGIOTENSIN I.
CC FT PEPTIDE 25 32 ANGIOTENSIN II.
CC FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 476 AA; 51304 MW; CBA517CD9FA029F7 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6
Db 26 RVIHP 31

RESULT 5
ANGT_MOUSE
ID ANGT_MOUSE STANDARD; PRT; 477 AA.
AC P11859;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN SERPIN8 OR AGT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284703; PubMed=3397061;
RA Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT "Molecular cloning of the mouse angiotensinogen gene.";
RL Genomics 2:240-248(1988).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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DR PRINTS; PR00054; ANGIOTENSNGN.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; FALSE_NEG.
KW VASOCONSTRICTOR; GLYCOPROTEIN; Plasma; Serpin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 477 ANGIOTENSINOGEN.
FT PEPTIDE 25 34 ANGIOTENSIN I.
FT PEPTIDE 25 32 ANGIOTENSIN II.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 477 AA; 51990 MW; A877F4029F338607 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6
Db 26 RVIHP 31

RESULT 6
ANGT_RAT
ID ANGT_RAT STANDARD; PRT; 477 AA.
AC P01015;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN SERPIN8 OR AGT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=83169849; PubMed=6572971;
RA Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA Nakanishi S.;
RT "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN [2]
RP SEQUENCE OF 25-34.
RX MEDLINE=73060322; PubMed=4344907;
RA Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. II. Structure of rat
RT angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 20:1579-1581(1972).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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DR InterPro; IPR000227; Angiotensin.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR PRINTS; PR00654; ANGIOTENSNG.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; FALSE\_NEG.  
 KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 477 ANGIOTENSINOGEN.  
 FT PEPTIDE 25 34 ANGIOTENSIN I.  
 FT PEPTIDE 25 32 ANGIOTENSIN II.  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 477 AA; 51981 MW; 689051A5788D693D CRC64;

Query Match 100.0%; Score 35; DB 1; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVIYHP 6  
 |||||  
 Db 26 RVIYHP 31

RESULT 7  
 ANGT\_HUMAN STANDARD; PRT; 485 AA.  
 AC P01019; Q16358; Q16359;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
 GN SERPINA8 OR AGT  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RX MEDLINE=89170129; PubMed=2924688;  
 RA Gaillard I., Clausen E., Corvol P.;  
 RT "Structure of human angiotensinogen gene."  
 RL DNA 8:87-99(1989).  
 RN [2]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=85000455; PubMed=6089875;  
 RA Kageyama K., Ohkubo H., Nakanishi S.;  
 RT "Primary structure of human preangiotensinogen deduced from the  
 RT cloned cDNA sequence."  
 RL Biochemistry 23:3603-3609(1984).  
 RN [3]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=90237063; PubMed=1692023;  
 RA Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,  
 RA Murakami K.;  
 RT "Structure and expression of the human angiotensinogen gene.  
 RT Identification of a unique and highly active promoter."  
 RL J. Biol. Chem. 265:7576-7582(1990).  
 RN [4]  
 RX SEQUENCE OF 1-338 FROM N.A.  
 RX MEDLINE=87244745; PubMed=2885106;  
 RA Kunapuli S.P., Kumar A.;  
 RT "Molecular cloning of human angiotensinogen cDNA and evidence for the  
 RT presence of its mRNA in rat heart."  
 RL Circ. Res. 60:786-790(1987).  
 RN [5]  
 RX SEQUENCE OF 34-45, AND SUBUNITS.  
 RX MEDLINE=95293954; PubMed=7539791;  
 RA Ovig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,  
 RA Stigbrand T., Gleich G.J., Sottrup-Jensen L.;  
 RT "Identification of angiotensinogen and complement C3dg as novel

RT proteins binding the proform of eosinophil major basic protein in  
 RT human pregnancy serum and plasma."  
 RL J. Biol. Chem. 270:13645-13651(1995).  
 RN [6]  
 RX SEQUENCE OF 34-43.  
 RX MEDLINE=69014170; PubMed=4300938;  
 RA Arakawa K., Minohara A., Yamada J., Nakamura M.;  
 RT "Enzymatic degradation and electrophoresis of human angiotensin I."  
 RL Biochim. Biophys. Acta 168:106-112(1968).  
 RN [7]  
 RP STRUCTURE BY NMR OF ANGIOTENSIN II.  
 RX MEDLINE=98151281; PubMed=9492317;  
 RA Carpenter K.A., Wilkes B.C., Schiller P.W.;  
 RT "The octapeptide angiotensin II adopts a well-defined structure in a  
 RT phospholipid environment."  
 RL Eur. J. Biochem. 251:448-453(1998).  
 RN [8]  
 RP VARIANTS MET-207; THR-268 AND CYS-281.  
 RX MEDLINE=93008239; PubMed=1394429;  
 RA Jeunemaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,  
 RA Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,  
 RA Lalouel J.-M., Corvol P.;  
 RT "Molecular basis of human hypertension: role of angiotensinogen."  
 RL Cell 71:169-180(1992).  
 RN [9]  
 RP VARIANT THR-268.  
 RX MEDLINE=93291876; PubMed=8513325;  
 RA Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,  
 RA Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,  
 RA Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;  
 RT "A molecular variant of angiotensinogen associated with  
 RT preclampsia."  
 RL Nat. Genet. 4:59-61(1993).  
 RN [10]  
 RP VARIANTS ILB-242; ARG-244 AND CYS-281.  
 RX MEDLINE=95331754; PubMed=7607642;  
 RA Hixson J.E., Powers P.K.;  
 RT "Detection and characterization of new mutations in the human  
 RT angiotensinogen gene (AGT)."  
 RL Hum. Genet. 96:110-112(1995).  
 CC [-] FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC [-] SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2  
 CC heterotetramer with the proform of PRG2 and as a complex (probably  
 CC a 2:2:2 heterohexamer) with pro-PRG2 and C3dg.  
 CC [-] TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC [-] DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO  
 CC ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION  
 CC (PIH) (PRECLAMPSIA).  
 CC [-] SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 CC [-] CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.  
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 CC -----  
 CC EMBL; K02215; AAA51731.1; -;  
 CC EMBL; M24689; AAA51679.1; -;  
 CC EMBL; M24686; AAA51679.1; JOINED.  
 CC EMBL; M24687; AAA51679.1; JOINED.  
 CC EMBL; M24688; AAA51679.1; JOINED.  
 CC EMBL; X15324; CAA33385.1; -;  
 CC EMBL; X15325; CAA33385.1; JOINED.  
 CC EMBL; X15326; CAA33385.1; JOINED.  
 CC EMBL; X15327; CAA33385.1; JOINED.



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DR EMBL; M69110; AAA52282.1; -
DR EMBL; S78529; AAD14287.1; -
DR EMBL; S78530; AAD14288.1; -
DR PIR; A01249; ANHU
DR PIR; A31362; A31362.
DR PIR; A35203; A35203.
DR SWISS-2DPAGE; P01019; HUMAN.
DR MM; 106150; -
DR InterPro; IPR000227; Angiotensngn.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PRINTS; PR00654; ANGIOTENSNGN.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
KW Disease mutation; Polymorphism.
FT SIGNAL 1 33
FT CHAIN 34 485
FT PEPTIDE 34 43
FT PEPTIDE 34 41
FT CARBOHYD 47 47
FT CARBOHYD 170 170
FT CARBOHYD 304 304
FT CARBOHYD 328 328
FT VARIANT 207 207
FT VARIANT 242 242
FT VARIANT 244 244
FT VARIANT 268 268
FT VARIANT 281 281
FT CONFLICT 333 333
FT SEQUENCE 485 AA; 53154 MW; 5026C2DFB2DD236E CRC64;

Query Match 100.0%; Score 35; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6
DB 35 RVIYHP 40
|||||

RESULT 8
TX18_HUMAN
ID TX18_HUMAN STANDARD; PRT; 501 AA.
AC O95935; O9UJ16;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-box transcription factor TBX18 (T-box protein 18) (Fragment).
GN TBX18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bates K.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 42-223 FROM N.A.
RX MEDLINE=99107806; PubMed=9888994;
RA Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA Armstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT "Identification, mapping and phylogenomic analysis of four new human
RL members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19."
RL Genomics 55:10-20(1999).
CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN

```

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CC DEVELOPMENTAL PROCESSES.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL035694; CAB45196.1; -
CC EMBL; AJ010278; CAB37937.1; -
CC HSP; P24781; IYBR.
CC MM; 604613; -
CC InterPro; IPR001699; T-box.
CC Pfam; PF00907; T-box; 1.
CC PRINTS; PR00937; TBOX.
CC SMART; SM00425; TBOX; 1.
CC PROSITE; PS01283; TBOX_1; 1.
CC PROSITE; PS01264; TBOX_2; 1.
CC PROSITE; PS0252; TBOX_3; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND 42 224
FT SEQUENCE 501 AA; 54229 MW; 45A732B009A4E5F5 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6
DB 115 RVIYHP 120
|||||

RESULT 9
TBX6_MOUSE
ID TBX6_MOUSE STANDARD; PRT; 540 AA.
AC P70327;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-box transcription factor TBX6 (T-box protein 6).
GN TBX6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97032942; PubMed=8878690;
RA Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,
RA Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;
RT "Evolution of mouse T-box genes by tandem duplication and cluster
RT dispersion."
RL Genetics 144:249-254(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastrula;
RX MEDLINE=97115702; PubMed=8954725;
RA Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;
RT "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at
RT gastrulation."
RL Dev. Biol. 180:534-542(1996).
RN [3]
RP FUNCTION.
RX MEDLINE=98140705; PubMed=9490412;
RA Chapman D.L., Papaioannou V.E.;
RT "Three neural tubes in mouse embryos with mutations in the T-box gene

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EMBL: AF306666; AAG48598.1; -;  
MGI:1923615; Tbx18.  
InterPro: IPR001699; T-box.  
Pfam: PF00907; T-box; 1.  
PRINTS: PR00937; TBOX.  
SMART: SM00425; TBOX; 1.  
PROSITE: PS01283; TBOX\_1; 1.  
PROSITE: PS01264; TBOX\_2; 1.  
PROSITE: PS02552; TBOX\_3; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DNA\_BIND 149 336 T-BOX.  
SQ SEQUENCE 613 AA; 65463 MW; A9E64D395725AB38 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 613;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
Db 227 RVIYHP 232  
|||||

RESULT 12  
ANGI\_BOTJA STANDARD; PRT; 10 AA.  
AC Q10581;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide I (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.

TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
RT "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca."  
RL Comp. Biochem. Physiol. 113B:467-473(1996).  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 97.1%; Score 34; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.16;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
Db 2 RVIYHP 7  
|||||

RESULT 13  
ANGT\_BOVIN STANDARD; PRT; 10 AA.  
AC P01017;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).

GN SERPINA8 OR AGT.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RA Elliott D.F., Peart W.S.;  
RT "The amino acid sequence in a hypertensin."  
RL Biochem. J. 65:246-254(1957).  
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.  
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR PIR; A01250; A01250.  
DR PIR; A90345; A90345.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1282 MW; CEEFDD761F2DB42 CRC64;

Query Match 97.1%; Score 34; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.16;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIYHP 6  
Db 2 RVIYHP 7  
|||||

RESULT 14  
ANGT\_CHICK STANDARD; PRT; 10 AA.  
AC P01018;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
GN SERPINA8 OR AGT.  
OS Gallus gallus (Chicken), and  
OS Coturnix coturnix japonica (Japanese quail).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031, 93934;  
RN [1]  
RP SEQUENCE.

SPECIES=Chicken;  
RX MEDLINE=74127845; PubMed=4361802;  
RA Nakayama T., Nakajima T., Sokabe H.;  
RT "Comparative studies on angiotensins. 3. Structure of fowl angiotensin and its identification by DNS-method."  
RL Chem. Pharm. Bull. 21:2085-2087(1973).  
RN [2]  
RP SEQUENCE.

SPECIES=C.c.japonica;  
RX MEDLINE=90284684; PubMed=2191893;  
RA Takei Y., Hasegawa Y.;  
RT "Vasopressor and depressor effects of native angiotensins and inhibition of these effects in the Japanese quail."  
RL Gen. Comp. Endocrinol. 79:12-22(1990).  
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE

CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -I- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR: A01250; A01250.  
DR PIR: A90917; A90917.  
DR PIR: A60624; A60624.  
DR PROSITE: IPR000215; Serpin.  
DR VASOCONSTRICTOR; Plasma; Serpin.  
KW VASOCONSTRICTOR; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1232 MW; CEPBDD761F2DB42 CRC64;

Query Match 97.1%; Score 34; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.16;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RVIYHP 6  
|||:|  
Db 2 RVIYHP 7

RESULT 15  
ANGT\_CRIGE STANDARD; PRT; 11 AA.  
AC P09037;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Crinia-angiotensin II.  
OS Crinia georgiana (Quacking frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Crinia.  
OX NCBI\_TaxID=8374;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin;  
RX MEDLINE=80024575; PubMed=488254;  
RA Erspaner V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;  
RT "Amino acid composition and sequence of crinia-angiotensin, an  
RT angiotensin II-like endecapeptide from the skin of the Australian  
RT frog Crinia georgiana";  
RL Experientia 35:1132-1133(1979).  
DR PIR: S07207; S07207.  
KW VASOCONSTRICTOR.  
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 94.3%; Score 33; DB 1; Length 11;  
Best Local Similarity 66.7%; Pred. No. 0.29;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RVIYHP 6  
|||:|  
Db 5 RVIYHP 10

Search completed: July 1, 2002, 07:47:07  
Job time: 473 sec

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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:10 ; Search time 122.73 seconds  
(without alignments)  
8.457 Million cell updates/sec

Title: US-09-723-197-5  
Perfect score: 35  
Sequence: 1 RVIHP 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	14	5 Q10757	Q10757 theromyzon
2	35	100.0	245	6 Q95J13	Q95J13 pan troglod
3	35	100.0	295	4 Q9HA44	Q9HA44 homo sapien
4	35	100.0	436	11 Q9CSJ0	Q9CSJ0 mus musculu
5	35	100.0	461	11 Q9D2V0	Q9D2V0 mus musculu
6	35	100.0	477	4 Q96FD5	Q96FD5 homo sapien
7	35	100.0	485	4 Q96F91	Q96F91 homo sapien
8	35	100.0	485	6 Q9GLP7	Q9GLP7 pan troglod
9	35	100.0	485	6 Q9GLP6	Q9GLP6 gorilla gor
10	35	100.0	485	6 Q9GLN8	Q9GLN8 pan troglod
11	35	100.0	486	6 Q9TS20	Q9TS20 callithrix
12	35	100.0	533	4 Q96SF7	Q96SF7 homo sapien
13	34	97.1	10	13 Q9PS07	Q9PS07 alligator m
14	34	97.1	175	5 Q9GQEA	Q9GQEA branchiosto
15	34	97.1	183	5 Q9GQEB	Q9GQEB branchiosto
16	34	97.1	316	2 Q9Z5B8	Q9Z5B8 streptomyc

17	34	97.1	624	5	Q966RS	Q966RS branchiosto
18	33	94.3	249	13	Q9W701	Q9W701 paralichthy
19	33	94.3	694	2	Q9EWA5	Q9EWA5 streptomyc
20	33	94.3	1094	2	Q93H78	Q93H78 streptomyc
21	32	91.4	130	13	Q90WR1	Q90WR1 oryzias lat
22	32	91.4	171	17	Q97IG2	Q97IG2 sulfobus
23	32	91.4	174	5	Q9GQEA	Q9GQEA branchiosto
24	32	91.4	179	5	Q9GQEB	Q9GQEB branchiosto
25	32	91.4	182	13	Q93357	Q93357 gallus gall
26	32	91.4	194	13	Q90WR0	Q90WR0 oryzias lat
27	32	91.4	290	11	Q9D533	Q9D533 mus musculu
28	32	91.4	382	5	Q9U3J6	Q9U3J6 caenorhabdi
29	32	91.4	382	13	Q97317	Q97317 gallus gall
30	32	91.4	410	12	Q9GQF8	Q9GQF8 cullex nigri
31	32	91.4	420	5	P90985	P90985 caenorhabdi
32	32	91.4	437	13	Q9DDU4	Q9DDU4 brachydanio
33	32	91.4	580	12	Q919R0	Q919R0 cullex nigri
34	32	91.4	588	13	Q9PVX4	Q9PVX4 cynops pyrr
35	32	91.4	591	13	Q9PVX2	Q9PVX2 cynops pyrr
36	32	91.4	608	13	Q9PVX3	Q9PVX3 cynops pyrr
37	32	91.4	672	13	Q9W7B7	Q9W7B7 brachydanio
38	32	91.4	687	13	Q9IAL0	Q9IAL0 brachydanio
39	32	91.4	688	13	Q9W7R7	Q9W7R7 xenopus lae
40	32	91.4	688	13	Q9IBC8	Q9IBC8 xenopus lae
41	32	91.4	695	5	Q9XUQ0	Q9XUQ0 caenorhabdi
42	32	91.4	711	13	Q9IBC7	Q9IBC7 xenopus lae
43	32	91.4	716	13	Q9PUM1	Q9PUM1 xenopus lae
44	32	91.4	808	5	Q966Q2	Q966Q2 ciona lntes
45	31	88.6	87	13	Q9PUS8	Q9PUS8 brachydanio

## ALIGNMENTS

RESULT 1

ID	Q10757	PRELIMINARY;	PRT;	14 AA.
AC	Q10757;			
DT	01-NOV-1996 (TREMREL. 01, Created)			
DT	01-NOV-1996 (TREMREL. 01, Last sequence update)			
DE	01-NOV-1998 (TREMREL. 08, Last annotation update)			
DE	ANGIOTENSINOGEN (FRAGMENT).			
OS	Theromyzon tessulatum (Leech).			
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;			
OC	Rhynchobdellida; Glossiphoniidae; Theromyzon.			
OX	NCBI_TaxID=13286;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=95365039; PubMed=7637887;			
RA	Laurent V., Bulet P., Salzet M.A.;			
RT	"A comparison of the leech Theromyzon tessulatum angiotensin I-like			
RT	molecule with forms of vertebrate angiotensinogens: a hormonal system			
RL	conserved in the course of evolution."			
RL	Neurosci. Lett. 190:175-178(1995).			
RN	[2]			
RP	SEQUENCE OF 1-10.			
RC	TISSUE-BRAIN;			
RX	MEDLINE=96201949; PubMed=8612806;			
RA	Laurent V., Salzet M.;			
RT	"Metabolism of angiotensins by head membranes of the leech Theromyzon			
RT	tessulatum."			
RL	FEBS Lett. 384:123-127(1996).			
CC	!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.			
KW	Glycoprotein; Serpin.			
FT	NON_TER 14			
SQ	SEQUENCE 14 AA; 1763 MW; 335109D8EEFBDD7 CRC64;			

Query Match 100.0%; Score 35; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.99;  
Matches: 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RVIHP 6

```
Db 2 RVYIHP 7
|||||
RESULT 2
Q95J13 PRELIMINARY; PRT; 245 AA.
AC Q95J13;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
GN REN.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504, AND 505;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062027; BAB55856.1; -.
DR EMBL; AB062028; BAB55857.1; -.
FT NON_TER 245
SQ SEQUENCE 245 AA; 26317 MW; E0092390B9803E0B CRC64;

Query Match 100.0%; Score 35; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVYIHP 6
|||||
Db 35 RVYIHP 40

RESULT 3
Q9HA44 PRELIMINARY; PRT; 295 AA.
AC Q9HA44;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ12268 FIS, CLONE MAMMAL001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE TRANSCRIPTION FACTOR TBX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9608;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuna M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022330; BAB14014.1; -.
DR HSSP; P24781; 1XBR.
DR InterPro: IPR001699; T-box.
DR Pfam: PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS50252; TBOX_3; 1.
SQ SEQUENCE 295 AA; 33197 MW; F2BD3E53E0ED21E0 CRC64;

Query Match 100.0%; Score 35; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVYIHP 6
|||||
Db 35 RVYIHP 40

RESULT 3
Q9HA44 PRELIMINARY; PRT; 295 AA.
AC Q9HA44;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ12268 FIS, CLONE MAMMAL001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE TRANSCRIPTION FACTOR TBX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9608;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuna M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022330; BAB14014.1; -.
DR HSSP; P24781; 1XBR.
DR InterPro: IPR001699; T-box.
DR Pfam: PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS50252; TBOX_3; 1.
SQ SEQUENCE 295 AA; 33197 MW; F2BD3E53E0ED21E0 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVYIHP 6
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Db 171 RVYIHP 176

RESULT 4
Q9CSJ0 PRELIMINARY; PRT; 436 AA.
ID Q9CSJ0;
AC Q9CSJ0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 2810012F10RIK PROTEIN (FRAGMENT).
GN TBX18 OR 2810012F10RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK012723; BAB28434.1; -.
DR HSSP; P24781; 1XBR.
DR MGD; MGI:1923615; Tbx18.
DR InterPro: IPR001699; T-box.
DR Pfam: PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS50252; TBOX_3; 1.
FT NON_TER 1
SQ SEQUENCE 436 AA; 47478 MW; 8770E4F482CFC13A CRC64;

Query Match 100.0%; Score 35; DB 11; Length 436;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVYIHP 6
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Db 50 RVYIHP 55

RESULT 5
Q9D2V0 PRELIMINARY; PRT; 461 AA.
ID Q9D2V0
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Q9D2V0;  
01-JUN-2001 (TREMBLrel. 17, Created)  
01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN.  
GN AGT.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK018763; BAB31393.1; -;  
DR MGD: MGI:87963; Agt.  
DR InterPro: IPR000227; Angiotensngn.  
DR InterPro: IPR000215; Serpin.  
DR PRINTS: PR00654; ANGIOTENSNGN.  
DR SMART: SM00093; SERPIN; 1.  
SQ SEQUENCE 461 AA; 50327 MW; 446EB0881079251F CRC64;

Query Match 100.0%; Score 35; DB 11; Length 461;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
| | | | |  
DB 31 RVIHP 36

RESULT 6  
Q96FD5  
ID Q96FD5 PRELIMINARY; PRT; 477 AA.  
AC Q96FD5;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE SIMILAR TO ANGIOTENSINOGEN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRN, AND GLOBULASTOMA WITH EGFR AMPLIFICATION;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC011231; AAH11231.1; -;  
SQ SEQUENCE 477 AA; 51985 MW; AB79B8B70592FDE2 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 477;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
| | | | |  
DB 26 RVIHP 31

RESULT 7  
Q96F91  
ID Q96F91 PRELIMINARY; PRT; 485 AA.  
AC Q96F91;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN (SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE  
DE A (ALPHA-1 ANTITRYPSIN, MEMBER 8).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRN, AND GLOBULASTOMA WITH EGFR AMPLIFICATION;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC011519; AAH11519.1; -;  
SQ SEQUENCE 485 AA; 53114 MW; 50BA5E9DCD4C8E7F CRC64;

Query Match 100.0%; Score 35; DB 4; Length 485;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
| | | | |  
DB 35 RVIHP 40

RESULT 8  
Q9GLP7  
ID Q9GLP7 PRELIMINARY; PRT; 485 AA.  
AC Q9GLP7;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN.  
GN AGT.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shattuck-Eidens D., McGrail M., Stone S.;  
RT "Germline mutations in the angiotensinogen gene cause predisposition  
RT to type 1 diabetes mellitus.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL: AF188487; AAG29056.1; -;  
DR InterPro: IPR000227; Angiotensngn.  
DR InterPro: IPR000215; Serpin.  
DR PRINTS: PR00654; ANGIOTENSNGN.  
DR SMART: SM00093; SERPIN; 1.  
DR PROSITE: PS00284; SERPIN; 1.  
KW Serpin.  
SQ SEQUENCE 485 AA; 53140 MW; 49EFB54AF31F8ADC CRC64;

Query Match 100.0%; Score 35; DB 6; Length 485;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RN [1]



RP SEQUENCE FROM N.A.  
RA Cobley V.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL357045; CAC39400.1;  
FT NON\_TER 1  
SQ SEQUENCE 533 AA; 58308 MW; 7EC5008CEE275A9 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 533;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 126 RVIHP 131

## RESULT 13

Q9PS07 PRELIMINARY; PRT; 10 AA.  
AC Q9PS07;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)  
DE ANGIOTENSIN I, ANG I.  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93307610; PubMed=8319878;  
RA Takel Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,  
RA Stephens G.A., Sakakibara S.;  
RT "New angiotensin I isolated from a reptile, Alligator  
RT mississippiensis."  
RL Gen. Comp. Endocrinol. 90:214-219(1993).  
SQ SEQUENCE 10 AA; 1216 MW; CEE38DD761F2DB42 CRC64;

Query Match 97.1%; Score 34; DB 13; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.1;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 2 RVIHP 7

## RESULT 14

Q9GQE4 PRELIMINARY; PRT; 175 AA.  
AC Q9GQE4;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE T-BOX PROTEIN AMPHIOXUS/TBRL/TBX21 (FRAGMENT)  
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).  
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
OC Branchiostoma.  
OX NCBI\_TaxID=7739;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20519458; PubMed=11063699;  
RA Ruvinsky I., Silver L.M., Gibson-Brown J.J.;  
RT "Phylogenetic analysis of T-Box genes demonstrates the importance of  
RT amphioxus for understanding evolution of the vertebrate genome."  
RL Genetics 156:1249-1257(2000).  
DR EMBL; AF262568; AAG34893.1;  
DR HSSP; P24781; IXHR.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00937; T-box.  
DR PRINTS; PR00937; TBOX.

DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
FT NON\_TER 1  
SQ SEQUENCE 175 AA; 20057 MW; 95D34C4996A0DD6B CRC64;

Query Match 97.1%; Score 34; DB 5; Length 175;  
Best Local Similarity 83.3%; Pred. No. 19;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 73 RVIHP 78

## RESULT 15

Q9GQE6 PRELIMINARY; PRT; 183 AA.  
AC Q9GQE6;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE T-BOX PROTEIN AMPHIOXUS/TBRL/TBX21 (FRAGMENT)  
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).  
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
OC Branchiostoma.  
OX NCBI\_TaxID=7739;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20519458; PubMed=11063699;  
RA Ruvinsky I., Silver L.M., Gibson-Brown J.J.;  
RT "Phylogenetic analysis of T-Box genes demonstrates the importance of  
RT amphioxus for understanding evolution of the vertebrate genome."  
RL Genetics 156:1249-1257(2000).  
DR EMBL; AF262566; AAG34891.1;  
DR HSSP; P24781; IXHR.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00937; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 183  
SQ SEQUENCE 183 AA; 21027 MW; F01E0579067071FD CRC64;

Query Match 97.1%; Score 34; DB 5; Length 183;  
Best Local Similarity 83.3%; Pred. No. 19;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVIHP 6  
Db 74 RVIHP 79

Search completed: July 1, 2002, 07:45:11  
Job time: 407 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 Seconds  
(without alignments)  
3.509 Million cell updates/sec

Title: US-09-723-197-6  
Perfect score: 30  
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	5	17 AAR95667	Angiotensin II fra
2	30	100.0	5	18 AAW33326	Targetting conjuga
3	30	100.0	5	18 AAW33018	Targetting conjuga
4	30	100.0	5	18 AAW11210	Targetting conjuga
5	30	100.0	5	18 AAW14984	Conjugating peptid
6	30	100.0	5	19 AAW65602	Angiotensin II ana
7	30	100.0	5	19 AAW64733	Angiotensin II pep
8	30	100.0	5	19 AAW71115	Peptide AII(3-7) u
9	30	100.0	5	20 AAY49591	Angiotensin analog
10	30	100.0	5	20 AAY33906	Angiotensin II ana
11	30	100.0	5	20 AAY30544	Amino acid sequenc

12	30	100.0	5	20 AAY30588	Amino acid sequenc
13	30	100.0	5	20 AAY32719	Angiotensin II ana
14	30	100.0	5	20 AAY33773	Angiotensin II (AI
15	30	100.0	5	20 AAY15350	Angiotensin II (AI
16	30	100.0	5	20 AAY15310	Angiotensin II (AI
17	30	100.0	5	21 AAB27406	Angiotensin II ana
18	30	100.0	5	21 AAB28104	Angiotensin II ana
19	30	100.0	5	21 AAY84129	Peptide comprising
20	30	100.0	5	21 AAY77042	Angiotensin II (AI
21	30	100.0	5	21 AAY57406	Angiotensin peptid
22	30	100.0	5	22 AAE08876	AII peptide (resid
23	30	100.0	5	22 AAE02993	Human angiotensin
24	30	100.0	5	22 AAE03156	Human angiotensin
25	30	100.0	6	17 AAR95664	Angiotensin II fra
26	30	100.0	6	17 AAR95666	Angiotensin II fra
27	30	100.0	6	18 AAW33325	Targetting conjuga
28	30	100.0	6	18 AAW32605	Angiotensin IV ant
29	30	100.0	6	18 AAW32609	D-Vall-Angiotensin
30	30	100.0	6	18 AAW33017	Targetting conjuga
31	30	100.0	6	18 AAW11209	Targetting conjuga
32	30	100.0	6	18 AAW14983	Conjugating peptid
33	30	100.0	6	18 AAW14124	Angiotensin IV ant
34	30	100.0	6	19 AAW65599	Angiotensin II ana
35	30	100.0	6	19 AAW65601	Angiotensin II ana
36	30	100.0	6	19 AAW64730	Angiotensin II pep
37	30	100.0	6	19 AAW64732	Angiotensin II pep
38	30	100.0	6	19 AAW71112	Peptide AII(3-8) u
39	30	100.0	6	19 AAW71114	Peptide AII(2-7) u
40	30	100.0	6	19 AAW65540	Peptide motif havi
41	30	100.0	6	20 AAY49588	Angiotensin analog
42	30	100.0	6	20 AAY49590	Angiotensin analog
43	30	100.0	6	20 AAY50297	Neutrophil-activat
44	30	100.0	6	20 AAY33903	Angiotensin II ana
45	30	100.0	6	20 AAY33905	Angiotensin II ana

## ALIGNMENTS

## RESULT 1

AAR95667  
ID AAR95667 standard; peptide; 5 AA.  
AC AAR95667;  
DT 09-JAN-1997 (first entry)  
DE Angiotensin II fragment AII(3-7).  
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;  
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;  
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.  
XX Synthetic.  
XX OS  
XX WO9614858-A1.  
XX PD 23-MAY-1996.  
XX PF 14-NOV-1995; 95WO-US14764.  
XX PR 06-JUN-1995; 95US-0465775.  
XX PR 14-NOV-1994; 94US-0337781.  
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX Dizerega GS, Rodgers K;  
XX WPI; 1996-259561/26.  
XX Accelerating wound healing by application of angiotensin II  
XX fragments - are effective at very low concn. and do not cause  
XX hypertension

XX PS Disclosure; Page 4; 46pp; English.

XX CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see

XX CC AAR95662) is an octapeptide present in humans and other species. AT2 is

CC one of the most potent vasoconstrictors known, causing constriction of

CC the arterioles. The formation of angiotensin is initiated by the action

CC of renin on angiotensinogen. The substance formed is a decapeptide

CC called angiotensin I which is converted by the enzyme angiotensinase (by

CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release

CC of extracellular matrices involved in wound repair. These fragments can

CC be used in a compound for accelerating wound healing. The compounds are

CC administered as matrical or micellar solutions, formulated with a

CC carrier or diluent, alternatively the compound is applied in conjuncture

CC with a wound dressing. The carrier used in the composition is

CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly

CC glycols. By using fragments of this sequence (or analogues of it),

CC growth as well as healing of tissues is improved, such as in cases of

CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or

CC intraperitoneal surgical wounds. The compounds containing the AT2

CC fragments are less hypertensive than full length AT2, and are also

CC effective at much lower (nanomolar) concentrations than full length AT2.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
| | | | |

Db 1 vyihp 5

## RESULT 2

AAW33326  
ID AAW33326 standard; peptide; 5 AA.

XX AC AAW33326;

XX DT 05-FEB-1998 (first entry)

XX DE Targetting conjugate for bis-nicotinamide bifunctional chelator.

XX KW Bifunctional; bis-nicotinamide; chelator; radioactive; technetium;  
KW rhenum; conjugate; endothelin; angiotensin; targeting agent;  
KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
KW delivery.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9710853-A2.

XX PD 27-MAR-1997.

XX PF 19-SEP-1996; 96WO-DE01824.

XX PR 21-SEP-1995; 95DE-4036783.

XX PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.

XX PI Dinkelborg L, Hilger CS, Kramp W, Platzek J;

XX PI Raduechel B;

XX DR WPI; 1997-212562/19.

XX PT New bis-nicotinamide bi:functional chelating agents - forming new,  
PT stable technetium or rhenum complexes and conjugates useful as  
PT radiodiagnostic and radio:therapeutic agents

PS Claim 11; Page 42; 47pp; German.

XX CC Novel bis-nicotinamide bifunctional chelating agent for radioactive  
CC technetium and rhenum, when conjugated to an endothelin or  
CC angiotensin derived targeting agent, e.g. the present peptide, can  
CC be used for the in vivo imaging of organs, receptors and receptor  
CC containing tissues and/or atherosclerotic plaques, e.g. for the  
CC diagnosis of breast or prostatic carcinoma. They can also be used  
CC for cytostatic agent delivery.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
| | | | |

Db 1 vyihp 5

## RESULT 3

AAW333018  
ID AAW333018 standard; peptide; 5 AA.

XX AC AAW333018;

XX DT 26-JAN-1998 (first entry)

XX DE Targetting conjugate for bifunctional sulphonamide type ligand.

XX KW Bifunctional sulphonamide; ligand; radioactive; technetium;  
KW rhenum; conjugate; endothelin; angiotensin; targeting agent;  
KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
KW delivery.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN DE19536785-A1.

XX PD 27-MAR-1997.

XX PF 21-SEP-1995; 95DE-1036785.

XX PR 21-SEP-1995; 95DE-1036785.

XX PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.

XX PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;

XX PI Raduechel B;

XX DR WPI; 1997-193894/18.

XX PT Bifunctional sulphonamide type ligands for radioactive technetium or  
PT rhenum - and their chelates and conjugates, useful for imaging  
PT carcinoma or atherosclerosis

XX PS Claim 9; Page 12; 12pp; German.

XX CC Novel bifunctional sulphonamide type ligands for radioactive  
CC technetium and rhenum, when conjugated to an endothelin or  
CC angiotensin derived targeting agent, e.g. the present peptide, can  
CC be used for the in vivo imaging of organs, receptors and receptor  
CC containing tissues and/or atherosclerotic plaques, e.g. for the  
CC diagnosis of breast or prostatic carcinoma. They can also be used  
CC for cytostatic agent delivery.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
 Db 1 vylhp 5

## RESULT 4

AAW11210  
 ID AAW11210 standard; peptide; 5 AA.

XX AC AAW11210;

XX DT 26-JAN-1998 (first entry)

XX DE Targetting conjugate for bifunctional sulphonamide type ligand.

XX KW Bifunctional sulphonamide; ligand; radioactive; technetium;  
 KW rhenum; conjugate; endothelin; angiotensin; targeting agent;  
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
 KW delivery.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN DE19536780-A1.

XX PD 27-MAR-1997.

XX PF 21-SEP-1995; 95DE-1036780.

XX PR 21-SEP-1995; 95DE-1036780.

XX PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.

XX PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;  
 XX PI Raduechel B;

XX DR WPI; 1997-193892/18.

XX PT Bifunctional sulphonamide type ligands for radioactive technetium  
 PT and rhenum - and their chelates and conjugates with targeting  
 PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.

XX PS Claim 11; Page 19; 19pp; German.

XX CC Novel bifunctional sulphonamide type ligands for radioactive  
 CC technetium and rhenum, when conjugated to an endothelin or  
 CC angiotensin derived targeting agent, e.g. the present peptide, can  
 CC be used for the in vivo imaging of organs, receptors and receptor  
 CC containing tissues and/or atherosclerotic plaques, e.g. for the  
 CC diagnosis of breast or prostatic carcinoma. They can also be used  
 CC for cytostatic agent delivery.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
 Db 1 vylhp 5

## RESULT 5

AAW14984  
 ID AAW14984 standard; peptide; 5 AA.

XX

AC AAW14984;  
 XX DT 28-NOV-1997 (first entry)  
 XX DE Conjugating peptide for radio-therapeutic/diagnostic agent.

XX KW Conjugate; diseased tissue; endothelin; angiotensin; chemotactic;  
 KW radiodiagnostic; radiotherapeutic; diagnosis; tumour; ischaemia;  
 KW atherosclerosis; vascular disorder; ischemia.

XX OS Synthetic.

XX PN WO9710852-A2.

XX PD 27-MAR-1997.

XX PF 19-SEP-1996; 96WO-DE01821.

XX PR 21-SEP-1995; 95DE-4036781.

XX PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.

XX PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;  
 XX PI Raduechel B;

XX DR WPI; 1997-202627/18.

XX PT New sulphide-sulphonamide bi:functional chelating agents - forming  
 PT new, stable technetium or rhenum complexes and conjugates useful as  
 PT radiodiagnostic and radio-therapeutic agents

XX PS Claim 13; Page 45; 50pp; German.

XX CC XSNS-type bifunctional sulphide containing sulphonamide chelating  
 CC agents and their technetium or rhenum complexes, can form  
 CC covalently bonded conjugates with substances selectively enriched  
 CC in diseased tissue, e.g. the present peptide. The substance is an  
 CC endothelin or angiotensin peptide, or a partial sequence, analogue,  
 CC derivative or antagonist, or a chemotactic peptide.  
 CC The conjugates are radiodiagnostic or radiotherapeutic agents,  
 CC useful in the diagnosis of tumours, ischaemia or atherosclerotic  
 CC vascular disorders.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
 Db 1 vylhp 5

## RESULT 6

AAW65602  
 ID AAW65602 standard; peptide; 5 AA.

XX AC AAW65602;

XX DT 09-NOV-1998 (first entry)

XX DE Angiotensin II analogue, AII(3-7).

XX KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;  
 XX KW wound healing.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9826795-A1.

XX

PD 25-JUN-1998.  
 XX 16-DEC-1997; 97WO-US23461.  
 PF 15-DEC-1997; 97US-0990664.  
 PR 16-DEC-1996; 96US-0028310.  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PA Dizerega GS, Rodgers KE;  
 PI WPI; 1998-362518/31.  
 XX Promoting incorporation of skin graft onto underlying tissue -  
 PT comprises pre-treating graft with angiotensin II, or analogue or  
 PT peptide fragment  
 XX Disclosure; Page 6; 82pp; English.  
 PS The invention relates to the use of angiotensin II (AII), AII analogues,  
 CC AII fragments and AII fragment analogues for promoting incorporation of a  
 CC skin graft into underlying tissue of a mammal. The peptides are effective  
 CC in accelerating the growth or healing of skin grafts and in accelerating  
 CC re-epithelialisation and tissue repair, even at very low concentrations.  
 CC They can significantly accelerate the rate of healing at nanomolar levels  
 CC in vivo. AII accelerates wound repair by increased neovascularisation,  
 CC growth factor release, re-epithelialisation, extracellular matrix production  
 CC and increased flow of blood and nutrients to the injured tissue. Use of  
 CC the above peptides other than AII itself (an extremely potent vaso-  
 CC constrictor) may avoid the side-effects of AII, such as increase in blood  
 CC pressure and thirst. The present sequence represents an angiotensin  
 CC II fragment.  
 XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
 |||||  
 Db 1 vyihp 5

RESULT 7  
 AAW64733  
 ID AAW64733 standard; peptide; 5 AA.  
 XX AAW64733;  
 AC  
 DT 02-NOV-1998 (first entry)  
 XX Angiotensin II peptide #5.  
 DE  
 XX Proliferation; mesenchymal stem cell; lineage-specific cell;  
 KW haematopoietic; cell culture; transplantation; treatment; malignant;  
 KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9832457-A2.  
 PN 30-JUL-1998.  
 XX 26-JAN-1998; 98WO-US01552.  
 PF 23-JAN-1998; 98US-0066593.  
 XX 28-JAN-1997; 97US-0036507.  
 PR 08-MAY-1997; 97US-0046859.  
 PR 28-OCT-1997; 97US-0063684.  
 XX 31-OCT-1997; 97US-0063910.  
 PR

PR 18-NOV-1997; 97US-0065612.  
 XX 26-NOV-1997; 97US-0066593.  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 PI WPI; 1998-437044/37.  
 XX Promoting haematopoietic and mesenchymal cell proliferation and  
 PT differentiation - by contacting the cells with angiotensinogen,  
 PT angiotensin I or II, or analogues or fragments of these  
 XX Claim 7; Page 14; 114pp; English.  
 PS AAW64728-W64763 are peptides used in a novel method for accelerating the  
 CC proliferation of mesenchymal stem cells (MSCs), haematopoietic  
 CC lineage-specific cells or mesenchymal lineage-specific cells. The method  
 CC involves contacting the cells with an active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R1-R8 in  
 CC the sequence of formula R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together  
 CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,  
 CC Ala, Leu, norLeu, Ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane  
 CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoSer or  
 CC azatyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or  
 CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are  
 CC not defined in the specification, the peptide bond between Ra and Rb is  
 CC labile to aminopeptidase A cleavage excluding sequences including R4 as a  
 CC terminal Tyr group. A second active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R2-R8 in  
 CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,  
 CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also  
 CC described. The inventions are particularly useful in cell culture  
 CC mediums. These cells may be used in transplantation techniques for  
 CC treatment of malignant or inherited diseases. The formulae represent  
 CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),  
 CC or AII AT2 type 2 receptor agonists.  
 XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
 |||||  
 Db 1 vyihp 5

RESULT 8  
 AAW71115  
 ID AAW71115 standard; peptide; 5 AA.  
 XX AAW71115;  
 AC  
 XX 27-OCT-1998 (first entry)  
 DT Peptide AII(3-7) used to accelerate thermal wound healing.  
 DE  
 XX Angiotensin; AII; acceleration; thermal wound healing; human;  
 KW growth factor release; neovascularisation; re-epithelialisation;  
 KW extracellular matrix production.  
 XX Synthetic.  
 OS WO9833813-A2.  
 PN 06-AUG-1998.  
 XX 04-FEB-1998; 98WO-US02049.  
 PF 04-FEB-1997; 97US-0037166.  
 PR

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX DiZerega G, Rodgers KE;  
 XX WPI; 1998-437391/37.  
 XX Methods for accelerating thermal wound healing in humans - using  
 XX angiotensinogen II and AII analogues  
 XX Claim 3; Page 9; 58pp; English.  
 XX  
 CC AAW71110-27 represent peptide used in the method of the invention. The  
 CC specification describes a method of accelerating thermal wound healing  
 CC in humans. The method comprises applying to the thermally injured tissue  
 CC an amount of at least one active agent which comprises the peptides  
 CC AAW71115-27. The method can be used to promote the healing of thermal  
 CC wounds by accelerating growth factor release, neovascularisation,  
 CC re-epithelialisation and extracellular matrix production. The sequences  
 CC are analogues of the angiotensin or angiotensinogen family of proteins.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 30; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VYIHP 5  
 Db |  
 1 vyihp 5  
 RESULT 9  
 AAY49591  
 ID AAY49591 standard; peptide: 5 AA.  
 XX  
 AC AAY49591;  
 XX  
 DT 13-JAN-2000 (first entry)  
 XX  
 DE Angiotensin analogue peptide SEQ ID NO:6.  
 XX  
 KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;  
 KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.  
 XX Synthetic.  
 OS  
 XX W09952540-A1.  
 XX  
 XX 21-OCT-1999.  
 XX  
 XX 07-APR-1999; 99WO-US07654.  
 XX  
 XX 09-APR-1998; 98US-0081262.  
 XX  
 XX 12-JUN-1998; 98US-0089024.  
 XX  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 XX Rodgers KE, DiZerega G;  
 XX WPI; 1999-620285/53.  
 XX  
 XX Treating or preventing infections in mammals using peptides derived  
 XX from angiotensin or angiotensin receptor agonists  
 XX Claim 2; Page 10; 91pp; English.  
 XX  
 CC The present invention describes a method for treating or preventing  
 CC infections in mammals by administering peptides (A) that are fragments  
 CC or analogues (or their fragments) of angiotensinogen, angiotensins I or  
 CC II, or angiotensin II AT<sub>2</sub>-type receptor agonists. (A) contain at least  
 CC 3 consecutive amino acids (aa) from the sequence (S1):

CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;  
 CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane  
 CC carboxylic acid), Ala, dimethylglycine, pro, betaine, Glu(NH<sub>2</sub>), Gly,  
 CC Asp(NH<sub>2</sub>) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,  
 CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,  
 CC Ile, Gly, Pro, Alb (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr  
 CC (Optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;  
 CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;  
 CC R7 = pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =  
 CC sequences having R4 as a terminal Tyr residue are excluded. The method  
 CC is particularly used in cases of bacterial infection (e.g. septic shock,  
 CC peritonitis, bacteraemia or endotoxaemia) but also against viral and  
 CC parasitic infections. AAY49586 to AAY49623 represent specifically  
 CC claimed examples of (A).  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VYIHP 5  
 Db |  
 1 vyihp 5  
 RESULT 10  
 AAY33906  
 ID AAY33906 standard; peptide: 5 AA.  
 XX  
 AC AAY33906;  
 XX  
 DT 29-NOV-1999 (first entry)  
 XX  
 DE Angiotensin II analogue AII(3-7).  
 XX  
 KW embryonic stem cell; ES; angiotensin; totipotent cell;  
 KW gene therapy; replacement therapy; angiotensin II; AII;  
 KW analogue.  
 OS Homo sapiens.  
 XX  
 XX W09942122-A1.  
 XX  
 XX 26-AUG-1999.  
 XX  
 XX 16-FEB-1999; 99WO-US03243.  
 XX  
 XX 19-FEB-1998; 98US-0075179.  
 XX  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 XX DiZerega G, Rodgers KE;  
 XX WPI; 1999-527419/44.  
 XX  
 XX Promoting embryonal cell proliferation, using angiotensinogen and  
 XX angiotensin peptides, analogs or fragments  
 XX Claim 2; Page 8; 76pp; English.  
 XX  
 CC This is the amino acid sequence of the Angiotensin II analogue,  
 CC AII(3-7). The formation of Angiotensin II (AII) is initiated by the  
 CC action of renin on the plasma substrate angiotensinogen.  
 CC This results in Angiotensin I (AI) which then converted to AII by the  
 CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
 CC residues from AI (AAV42372).  
 CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and  
 CC analogs, Angiotensin II (AII), AII analogs, AII fragments, or AII  
 CC AT<sub>2</sub> type 2 receptor agonists can rapidly provide a large population of  
 CC ESCs (Embryonic Stem Cell) for use in replacement therapy. Similarly,  
 CC methods that increase in vivo proliferation of ESCs will enhance the

CC utility of replacement therapy by rapidly increasing local concentration  
CC of the stem cells and their progeny at the site of therapy.  
CC The method also increases the potential utility of ESCs as vehicles for  
CC gene therapy in certain disorders by more efficiently providing a large  
CC number of such cells for transfection, and also by providing a more  
CC efficient means to rapidly expand transduced ESCs.

XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

Db 1 vyihp 5

RESULT 11

AA30544

ID AAY30544 standard; peptide; 5 AA.

AC AAY30544;

DT 18-NOV-1999 (first entry)

DE Amino acid sequence of angiotensin II fragment AII3-7.

KW Angiotensin; analogue; tissue equivalent; cell proliferation.

OS Synthetic.

PN WQ9946285-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-0505261.

XX 11-MAR-1998; 98US-0077499.

XX 12-JUN-1998; 98US-0089064.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-551360/46.

XX An improved method for producing a tissue equivalent with angiotensin I  
PT and II derived active agents  
PS Claim 2; Page 54; 83pp; English.  
XX AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII  
CC fragments and AII analogues. The peptides are used in the method  
CC of the invention. The specification describes an improved method  
CC for producing a tissue equivalent. The method comprises contacting  
CC the tissue equivalent with angiotensin I and II derived active  
CC agents. The methods are used for production and culture of tissue  
CC equivalents (three-dimensional cell and tissue culture systems),  
CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,  
CC vascular graft, cartilage, ligament, collagen lattice, liver and  
CC kidney tissue equivalents. The methods and tissue culture systems  
CC are used for the long-term proliferation of cells and tissues  
CC in an in vitro environment that more closely approximates that found  
CC in vivo.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

Db 1 vyihp 5

RESULT 12

AA30588

ID AAY30588 standard; peptide; 5 AA.

XX AAY30588;

DT 18-NOV-1999 (first entry)

DE Amino acid sequence of an angiotensin II (AII) fragment AII3-7.

KW Angiotensin; analogue; radiation mitigation; tissue damage;

KW radiation therapy; bone marrow transplantation;

KW megakaryocyte production; platelet production; cancer therapy;

XX gene therapy; hematopoietic disorder.

XX Synthetic.

XX WQ9945945-A1.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US05194.

XX 10-MAR-1998; 98US-0077382.

XX 09-APR-1998; 98US-0081262.

XX 30-APR-1998; 98US-0083670.

XX 19-JUN-1998; 98US-0090096.

XX 22-JUN-1998; 98US-0090216.

XX 11-SEP-1998; 98US-0099557.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX (RODG/) RODGERS K E.

XX (DIZE/) DIZERECA G.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-551209/46.

XX Use of angiotensin and angiotensin type peptides, for mitigating  
PT radiation induced tissue damage, improving bone marrow transplantation  
PT and promoting megakaryocyte and platelet production  
PS Claim 2; Page 87; 116pp; English.

XX AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII  
CC fragments and AII analogues. The peptides are used in the method  
CC of the invention. The specification describes a method for mitigating  
CC radiation induced tissue damage, improving the effectiveness of  
CC radiation therapy, to support bone marrow transplantation, and  
CC promoting megakaryocyte production and mobilization and platelet  
CC production. The method comprises administration of the present peptides.  
CC The methods can be used to mitigate radiation induced tissue damage, to  
CC improve the effectiveness of radiation therapy, to support bone marrow  
CC transplantation, and to promote megakaryocyte production and  
CC mobilization and platelet production. They are used particularly in  
CC cancer therapy. They can also be used to provide megakaryocytes as  
CC vehicles for gene therapy in hematopoietic disorders, by providing a  
CC more efficient means to rapidly expand transduced megakaryocytes.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5



Db 1 vyihp 5  
|||||

## RESULT 13

AA32719  
ID AAY32719 standard; peptide: 5 AA.

AC AAY32719;

DT 09-NOV-1999 (first entry)

DE Angiotensin II analogue AII(3-7).

XX Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;  
KW chemotaxis; growth factor; liver regeneration; cirrhosis;  
KW hepatocarcinoma; hepatectomy; transplantation.

XX Synthetic.

OS Homo sapiens.

XX WO9939743-A2.

PD 12-AUG-1999.

XX 08-FEB-1999; 99WO-US02618.

PR 13-NOV-1998; 98US-0108412.

PR 09-FEB-1998; 98US-0074104.

XX (DIZE/) DIZEREGA G.

PA (RODG/) RODGERS K E.

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

PI Dizerega G, Rodgers KE;

XX WPI; 1999-508461/42.

XX Hepatic cell proliferation with angiotensin I and II derived active  
PT agents, useful for regeneration of liver after resection

PS Claim 2; Page 9; 66pp; English.

XX Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The  
CC peptides are derived from the AII peptide (AAY32750). AII increases  
CC mitogenesis and chemotaxis in cultured cells, and also increases the  
CC release of growth factors and extracellular matrices. AII has also been  
CC shown to increase the proliferation of certain cell types. The AII  
CC analogue peptides can be used as the active agent in a method for  
CC promoting hepatic cell proliferation and differentiation. The method  
CC involves contacting the hepatic cells with an amount effective enough to  
CC promote proliferation of any of the peptides. This method is useful in  
CC liver regeneration following resection of hepatocarcinomas, hepatitis  
CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic  
CC failure, hepatocyte transplantation, liver transplantation and other  
CC hepatic disorders where rapid regeneration of the liver is desirable. The  
CC methods are also useful in rapidly providing a large population of  
CC hepatic cells for use in cell therapy and for providing a large  
CC population of transsected hepatic cells for use in gene therapy.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

Db 1 vyihp 5  
|||||

## RESULT 14

AA33773

ID AAY33773 standard; peptide; 5 AA.

XX AAY33773;

DT 09-NOV-1999 (first entry)

DE Angiotensin II (AII) octapeptide fragment AII(3-7).

XX Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;  
KW neuronal cell proliferation; differentiation; Alzheimer's disease;  
KW Parkinson's disease; neuron replacement therapy.

XX Homo sapiens.

PN WO9942123-A1.

PD 26-AUG-1999.

XX 19-FEB-1999; 99WO-US03772.

XX 19-FEB-1998; 98US-0075232.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

PI Dizerega G, Rodgers KE;

XX WPI; 1999-527420/44.

XX Promoting neuronal cell proliferation and differentiation

PS Claim 2; Page 10; 62pp; English.

XX Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin  
CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The  
CC application of angiotensin to wound tissue significantly increases the  
CC rate of wound healing. AII is known to increase mitogenesis and  
CC chemotaxis in cultured cells, and also increases their release of growth  
CC factors and extracellular matrices, implicating it in cell growth and  
CC differentiation. AT2 receptors are receptors for AII and are thought to  
CC be involved in the mediation of the cell differentiation effects of AII.  
CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal  
CC cell proliferation or differentiation. This method is useful in the  
CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement  
CC therapy.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

Db 1 vyihp 5  
|||||

## RESULT 15

AA33773

ID AAY15350 standard; peptide; 5 AA.

XX AAY15350;

DT 09-NOV-1999 (first entry)

DE Angiotensin II (AII) analogue, AII(3-7).

XX burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;  
KW AII; analogue; chronic renal failure; cancer; bone marrow.

XX Synthetic.

OS Homo sapiens.

XX WO9940106-A2.  
 XX PN  
 XX 12-AUG-1999.  
 XX PD  
 XX PF 08-FEB-1999; 99WO-US02648.  
 XX PR 09-DEC-1998; 98US-0111535.  
 XX PR 09-FEB-1998; 98US-0074106.  
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PI Dizerega G, Rodgers KE;  
 XX WPI; 1999-508486/42.  
 XX DR  
 XX PT Promoting erythropoiesis with angiotensin I and II derived active  
 PT agents, useful for treatment of, e.g. congenital or acquired  
 PT aplastic or hypoplastic anemia  
 XX  
 XX PS Claim 2; Page 9; 76pp; English.  
 XX  
 XX This sequence is an angiotensin II (AII) analogue. Similar sequences  
 CC also based on the AII peptide have been tested against each other, AII  
 CC and a negative control. These active agents have been shown to affect  
 CC the levels of BFU-E (burst forming units-erythroid) in culture.  
 CC The active agents (AAV15348, AAV15359, AAV15372, AAV15379, and AAV15380)  
 CC augment erythropoiesis by potentiating erythropoietin-induced  
 CC differentiation. Increasing the rate of erythropoiesis improves clinical  
 CC benefits for the treatment of congenital or acquired aplastic or  
 CC hypoplastic anemia associated with chronic renal failure, end-stage renal  
 CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,  
 CC bone marrow transplantation and chronic diseases.  
 CC The active agents permit the use of smaller doses of erythropoietin  
 CC therefore decreasing treatment costs.  
 XX  
 XX SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VYIHP 5  
 Db 1 vyihp 5

Search completed: July 1, 2002, 07:41:55  
 Job time: 347 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:00 ; Search time 59.1 Seconds  
(without alignments)  
2.066 Million cell updates/sec

Title: US-09-723-197-6  
Perfect score: 30  
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	30	100.0	5	2	US-08-360-784B-27
2	30	100.0	5	2	US-08-465-775-6
3	30	100.0	5	3	US-09-054-308A-27
4	30	100.0	5	3	US-09-208-337-6
5	30	100.0	5	3	US-08-990-664-7
6	30	100.0	5	4	US-09-373-962-6
7	30	100.0	5	4	US-09-245-680-6
8	30	100.0	5	4	US-09-198-806C-6
9	30	100.0	5	4	US-09-352-191-6
10	30	100.0	5	4	US-09-012-400-6
11	30	100.0	6	1	US-08-113-292A-2
12	30	100.0	6	2	US-08-360-784B-1
13	30	100.0	6	2	US-08-360-784B-37
14	30	100.0	6	2	US-08-465-775-3
15	30	100.0	6	2	US-08-465-775-5
16	30	100.0	6	3	US-09-054-308A-1
17	30	100.0	6	3	US-09-054-308A-37
18	30	100.0	6	3	US-09-208-337-3
19	30	100.0	6	3	US-09-208-337-5
20	30	100.0	6	3	US-08-990-664-4
21	30	100.0	6	3	US-08-990-664-6
22	30	100.0	6	4	US-09-373-962-3
23	30	100.0	6	4	US-09-373-962-5
24	30	100.0	6	4	US-09-245-680-3
25	30	100.0	6	4	US-09-245-680-5
26	30	100.0	6	4	US-09-198-806C-3
27	30	100.0	6	4	US-09-198-806C-5

28	30	100.0	6	4	US-09-352-191-3	Sequence 3, Appli
29	30	100.0	6	4	US-09-352-191-5	Sequence 5, Appli
30	30	100.0	6	4	US-09-012-400-3	Sequence 3, Appli
31	30	100.0	6	4	US-09-012-400-5	Sequence 5, Appli
32	30	100.0	7	1	US-08-021-839A-4	Sequence 4, Appli
33	30	100.0	7	1	US-07-776-272-3	Sequence 3, Appli
34	30	100.0	7	1	US-08-337-781-3	Sequence 6, Appli
35	30	100.0	7	2	US-08-115-968-6	Sequence 3, Appli
36	30	100.0	7	2	US-08-115-968-9	Sequence 9, Appli
37	30	100.0	7	2	US-08-115-968-10	Sequence 10, Appli
38	30	100.0	7	2	US-08-115-968-11	Sequence 11, Appli
39	30	100.0	7	2	US-08-115-968-12	Sequence 12, Appli
40	30	100.0	7	2	US-08-115-968-13	Sequence 13, Appli
41	30	100.0	7	2	US-08-115-968-14	Sequence 14, Appli
42	30	100.0	7	2	US-08-115-968-15	Sequence 15, Appli
43	30	100.0	7	2	US-08-115-968-16	Sequence 16, Appli
44	30	100.0	7	2	US-08-360-784B-3	Sequence 3, Appli
45	30	100.0	7	2	US-08-360-784B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-08-360-784B-27  
; Sequence 27, Application US/08360784B  
; Patent No. 5854388  
; GENERAL INFORMATION:  
; APPLICANT: Harding, J.W.  
; TITLE OF INVENTION: Angiotensin IV Peptides and Receptor  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen O'Connor Johnson & Kindness  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,784B  
; FILING DATE: 22-DEC-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sheiness, Diana K.  
; REGISTRATION NUMBER: 35,356  
; REFERENCE/DOCKET NUMBER: WSUR-1-8113  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 224-0735  
; TELEFAX: (206) 224-0779  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Bos taurus  
; US-08-360-784B-27

Query Match 100.0%; Score 30; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 1 VYIHP 5

RESULT 2  
US-08-465-775-6  
; Sequence 6, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: diZerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-465-775-6

Query Match 100.0%; Score 30; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 1 VYIHP 5

RESULT 3  
US-09-054-308A-27  
; Sequence 27, Application US/09054308A  
; Patent No. 6022696  
; GENERAL INFORMATION:  
; APPLICANT: Harding, J.W.  
; APPLICANT: Wright, J.W.  
; TITLE OF INVENTION: Angiotensin IV Peptides and Receptor  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen O'Connor Johnson & Kindness  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101-2347

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/054,308A  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,784  
; FILING DATE: 22-DEC-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shelton, Dennis K.  
; REGISTRATION NUMBER: 26,997  
; REFERENCE/DOCKET NUMBER: WSUR110660  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 224-0718  
; TELEFAX: (206) 224-0779  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Bos taurus

US-09-054-308A-27

Query Match 100.0%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 1 VYIHP 5

RESULT 4  
US-09-208-337-6  
; Sequence 6, Application US/09208337  
; Patent No. 6096709  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: Gere, diZerega  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,337  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,775  
; FILING DATE: 06-JUN-1995

APPLICATION NUMBER: 08/337,781  
FILING DATE: 14-NOV-1994  
APPLICATION NUMBER: 08/126,368  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: USC010.001CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 949-760-0404  
TELEFAX: 949-760-9502  
TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-208-337-6

Query Match 100.0%; Score 30; DB 3; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

|||||

Db 1 VYIHP 5

RESULT 5

US-09-990-664-7

; Sequence 7, Application US/08990664

; Patent No. 6110895

; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen

; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: METHOD OF PROMOTING HEALING

; TITLE OF INVENTION: IN SKIN GRAFTS

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/990,664

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/028,310

; FILING DATE: 16-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER: USC012.001A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 714-760-0404

; TELEFAX: 714-760-9502

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-990-664-7

Query Match 100.0%; Score 30; DB 3; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

|||||

Db 1 VYIHP 5

RESULT 6

US-09-373-962-6

; Sequence 6, Application US/09373962

; Patent No. 6177407

; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen

; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue

; FILE REFERENCE: 98364A

; CURRENT APPLICATION NUMBER: US/09/373,962

; CURRENT FILING DATE: 1999-08-13

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:AI1 (3-7)

US-09-373-962-6

Query Match 100.0%; Score 30; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

|||||

Db 1 VYIHP 5

RESULT 7

US-09-245-680-6

; Sequence 6, Application US/09245680B

; Patent No. 6239109

; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen

; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Method of Promoting Erythropoiesis

; FILE REFERENCE: 98009B

; CURRENT APPLICATION NUMBER: US/09/245,680B

; CURRENT FILING DATE: 1999-02-08

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:AI1 (3-7)

US-09-245-680-6

Query Match 100.0%; Score 30; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

|||||

Db 1 VYIHP 5

## RESULT 8

US-09-198-806C-6

; Sequence 6, Application US/09198806C

; Patent No. 6248587

; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen

; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem

; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation

; FILE REFERENCE: 97,017-F1

; CURRENT APPLICATION NUMBER: US/09/198,806C

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: AII (3-7)

US-09-198-806C-6

Query Match

Best Local Similarity 100.0%; Score 30; DB 4; Length 5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

|||||

Db 1 VYIHP 5

## RESULT 9

US-09-352-191-6

; Sequence 6, Application US/09352191

; Patent No. 6258778

; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen

; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue

; TITLE OF INVENTION: Growth and Repair

; FILE REFERENCE: 983658

; CURRENT APPLICATION NUMBER: US/09/352,191

; CURRENT FILING DATE: 1999-07-12

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: AII (3-7)

US-09-352-191-6

Query Match

Best Local Similarity 100.0%; Score 30; DB 4; Length 5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

|||||

Db 1 VYIHP 5

## RESULT 10

US-09-012-400-6

; Sequence 6, Application US/09012400D

; Patent No. 6335195

; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen

; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell

; TITLE OF INVENTION: Proliferation and Differentiation

; FILE REFERENCE: 97,017-G

; CURRENT APPLICATION NUMBER: US/09/012,400D

; CURRENT FILING DATE: 1998-01-23

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: AII (3-7)

US-09-012-400-6

Query Match

Best Local Similarity 100.0%; Score 30; DB 4; Length 5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

|||||

Db 1 VYIHP 5

## RESULT 11

US-08-113-292A-2

; Sequence 2, Application US/08113292A

; Patent No. 5599663

; GENERAL INFORMATION:

; APPLICANT: Robert E. Vaughan

; TITLE OF INVENTION: ANGIOTENSIN IV AND ANALOGS AS

; TITLE OF INVENTION: REGULATORS OF FIBRINOLYSIS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/113,292A

; FILING DATE: August 27, 1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: John W. Freeman

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 05311/005001

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6

; TYPE: amino acid

; STRANDEDNESS: N/A

; TOPOLOGY: linear

US-08-113-292A-2

Query Match

Best Local Similarity 100.0%; Score 30; DB 1; Length 6;

Matches 100.0%; Pred. No. 1.7e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
|||||  
Db 1 VYIHP 5

## RESULT 12

US-08-360-784B-1  
; Sequence 1, Application US/08360784B  
; Patent No. 5854388  
; GENERAL INFORMATION:  
; APPLICANT: Harding, J.W.  
; TITLE OF INVENTION: Angiotensin IV Peptides and Receptor  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen O'Connor Johnson & Kindness  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101-2347

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,784B  
; FILING DATE: 22-DEC-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sheiness, Diana K...  
; REGISTRATION NUMBER: 35,356  
; REFERENCE/DOCKET NUMBER: WSUR-1-8113  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 224-0779  
; TELEFAX: (206) 224-0735

INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: Angiotensin IV  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Bos taurus

US-08-360-784B-1

Query Match 100.0%; Score 30; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
|||||  
Db 1 VYIHP 5

## RESULT 13

US-08-360-784B-37  
; Sequence 37, Application US/08360784B  
; Patent No. 5854388  
; GENERAL INFORMATION:  
; APPLICANT: Harding, J.W.  
; TITLE OF INVENTION: Angiotensin IV Peptides and Receptor  
; NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen O'Connor Johnson & Kindness  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101-2347

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,784B  
; FILING DATE: 22-DEC-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sheiness, Diana K...  
; REGISTRATION NUMBER: 35,356  
; REFERENCE/DOCKET NUMBER: WSUR-1-8113  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 224-0735  
; TELEFAX: (206) 224-0779

INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Bos taurus

US-08-360-784B-37

Query Match 100.0%; Score 30; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
|||||  
Db 1 VYIHP 5

## RESULT 14

US-08-465-775-3  
; Sequence 3, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-360  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-775-3

Query Match 100.0%; Score 30; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|  
|  
|  
|  
Db 1 VYIHP 5

RESULT 15  
US-08-465-775-5  
Sequence 5, Application US/08465775  
Patent No. 5955430  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen E.  
APPLICANT: dizerega, Gere S.  
TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: c/o Robbins, Berliner & Carson  
STREET: 201 No. 5955430th Figueroa Street #500  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90012  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,775  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-360  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-775-5

Query Match 100.0%; Score 30; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|  
|  
|  
|

Db 2 VYIHP 6  
Search completed: July 1, 2002, 07:43:00  
Job time: 301 sec



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**THIS PAGE BLANK (US770)**

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:28 ; Search time 69.93 seconds  
(without alignments)  
6.870 Million cell updates/sec

Title: US-09-723-197-6

Perfect score: 30

Sequence: 1 VYIHP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	10	2 S65432	angiotensin I - ho
2	30	100.0	14	2 A01250	angiotensin precu
3	30	100.0	15	2 A08334	angiotensin I prec
4	30	100.0	177	2 C71329	hypothetical prote
5	30	100.0	184	2 AC1584	hypothetical prote
6	30	100.0	349	2 T50372	probable ATP-depen
7	30	100.0	385	2 G84459	probable GDP-manno
8	30	100.0	415	2 G96778	hypothetical prote
9	30	100.0	423	1 A49125	gastrulation regul
10	30	100.0	432	1 A41056	brachyury homolog
11	30	100.0	436	1 S08156	gene T protein - m
12	30	100.0	444	2 T20803	hypothetical prote
13	30	100.0	476	1 JC2318	angiotensin precu
14	30	100.0	477	1 ANRT	angiotensin precu
15	30	100.0	477	1 A29978	angiotensin precu
16	30	100.0	485	1 ANHU	angiotensin precu
17	30	100.0	540	2 S72233	transcription fact
18	30	100.0	678	2 S14173	SIR1 protein - yea
19	30	100.0	695	2 T24950	hypothetical prote
20	30	100.0	759	2 A05777	molybdopterin-cont
21	30	100.0	968	2 T46568	ATP-dependent RNA
22	30	100.0	980	2 T39630	valine-tRNA ligase
23	30	100.0	982	2 T04542	hypothetical prote
24	30	100.0	1200	2 T15921	hypothetical prote
25	30	100.0	1220	2 A56236	probable RNA helic
26	30	100.0	1267	2 S35058	probable membrane
27	30	100.0	1355	1 VGBE11	149K glycoprotein
28	29	96.7	10	2 A06024	angiotensin I - Ja
29	29	96.7	10	2 A90917	angiotensin precu

#### ALIGNMENTS

##### RESULT 1

S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432

R:Wiljffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen  
Eur. J. Biochem. 237, 414-423, 1996  
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte  
A:Reference number: S65431; MUID:96215437  
A:Accession: S65432

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <WIJ>

A>Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 30; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

Db 3 VYIHP 7

##### RESULT 2

A01250

angiotensin precursor - horse (fragment)

C:Species: Equus caballus (domestic horse)

C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998

C:Accession: A92775; A01250

R:Skeggis Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.

J. Exp. Med. 106, 439-453, 1957

A:Reference number: A92775

A:Accession: A92775

A:Molecule type: protein

A:Residues: 1-14 <SKE>

C:Superfamily: antithrombin III

C:Keywords: blood pressure control; hormone; vasoconstrictor

F:1-10/Product: angiotensin I #status experimental <AN1>

F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 30; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

Db 3 VYIHP 7

angiotensin precu  
anti-angiotensin,  
hypothetical 16.1k  
probable acetyltra  
probable phosphino  
probable resistanc  
probable resistanc  
hypothetical prote  
galactose-binding  
Ribulose-5-Phospha  
hypothetical prote  
hypothetical prote  
lectin light chain  
galactose-inhibita  
conserved hypothet  
hypothetical prote

RESULT 3  
A60834  
angiotensin I precursor - dog (fragment)  
N;Alternate names: angiotensinogen I  
N;Contains: angiotensin I  
C;Species: Canis lupus familiaris (dog)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1998  
C;Accession: A60834  
R;Oliver, J.A.  
Hypertension 11, 21-27, 1988  
A;Title: Purification and partial characterization of canine angiotensinogen.  
A;Reference number: A60834; PMID:88113996  
A;Accession: A60834  
A;Molecule type: protein  
A;Residues: 1-15 <OLI>  
C;Superfamily: antithrombin III  
C;Keywords: glycoprotein; plasma  
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 30; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 3 VYIHP 7

RESULT 4  
C71329  
hypothetical protein TP0404 - syphilis spirochete  
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 05-Nov-1999  
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin-  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McBr-  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A;Reference number: A71250; PMID:98332770  
A;Accession: C71329  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-177 <COL>  
A;Cross-references: GB:AE001218; GB:AE000520; NID:g3322678; PIDN:AAC65395.1; PID:g332268  
A;Experimental source: strain Nichols  
C;Genetics:  
A;Gene: TP0404

Query Match 100.0%; Score 30; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 3 VYIHP 7

RESULT 5  
AC1584  
hypothetical protein lin1212 [imported] - Listeria innocua (strain Clip11262)  
C;Species: Listeria innocua  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: AC1584  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker-  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma-  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative genomics of Listeria species.  
A;Reference number: AB1077; PMID:21537279; PMID:11679669  
A;Accession: AC1584  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-184 <GLA>  
A;Cross-references: GB:AL592022; PIDN:CAC96443.1; PID:gl6413686; GSPDB:GN00178  
A;Experimental source: strain Clip11262  
C;Genetics:  
A;Gene: lin1212

Query Match 100.0%; Score 30; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 92 VYIHP 96

RESULT 6  
T50372  
probable ATP-dependent RNA helicase cdc28 [imported] - fission yeast (Schizosaccharom  
C;Species: Schizosaccharomyces pombe  
C;Date: 09-Jun-2000 #sequence\_revision 15-Sep-2000 #text\_change 17-Nov-2000  
C;Accession: T50372; T39792  
R;Skelton, J.; Churcher, C.M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, December 1999  
A;Reference number: Z25066  
A;Accession: T50372  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-262 <SKE>  
A;Cross-references: EMBL:AL135748; PIDN:CAB633784.1; GSPDB:GN00067; SPDB:SPBC874.01  
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.  
submitted to the EMBL Data Library, July 1999  
A;Reference number: Z21880  
A;Accession: T39792  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 229-349 <MCD>  
A;Cross-references: EMBL:AL109731; PIDN:CAB52028.1; GSPDB:GN00067; SPDB:SPBC19C2.01  
C;Genetics:  
A;Gene: SPBC19C2.01; SPDB:SPBC874.01  
A;Map position: 2

Query Match 100.0%; Score 30; DB 2; Length 349;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 284 VYIHP 288

RESULT 7  
G84459  
probable GDP-mannose pyrophosphorylase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C;Accession: G84459  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; PMID:20083487  
A;Accession: G84459  
A;Status: preliminary  
A;Molecule type: DNA

A:Residues: 1-385 <STO>  
A:Cross-references: GB:AE002093; NID:g4544432; PIDN:AAD22341.1; GSPDB:GNO0139  
C:Genetics:  
A:Gene: At2g04650  
A:Map position: 2

Query Match 100.0%; Score 30; DB 2; Length 385;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 292 VYIHP 296

RESULT 8

G96778  
hypotheoretical protein F9E10.24 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: G96778  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maili, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: G96778  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-415 <STO>  
A:Cross-references: GB:AE005173; NID:g6646773; PIDN:AAF21085.1; GSPDB:GNO0141  
C:Genetics:  
A:Gene: F9E10.24  
A:Map position: 1

Query Match 100.0%; Score 30; DB 2; Length 415;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 301 VYIHP 305

RESULT 9

A49125  
gastrulation regulatory protein Zf-T - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A49125  
R:Schulte-Merker, S.; Ho, R.K.; Herrmann, B.G.; Nusslein-Volhard, C.  
Development 116, 1021-1032, 1992  
A:Title: The protein product of the zebrafish homologue of the mouse T gene is expressed  
A:Reference number: A49125; MUID:93201989  
A:Accession: A49125  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-423 <SCH>  
A:Cross-references: GB:S57147; NID:g299316; PIDN:AAB25829.1; PID:g299317  
A:Experimental source: embryo  
A:Note: sequence extracted from NCBI backbone (NCBIN:127982, NCBIIP:127985)  
C:Superfamily: mouse gene T protein; T-box homology  
F:44-220/Domain: T-box homology <TBX>

Query Match 100.0%; Score 30; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 116 VYIHP 120

RESULT 10

A41056  
brachyury homology - African clawed frog  
N:Alternate names: gene T homolog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A41056  
R:Smith, J.C.; Price, B.M.J.; Green, J.B.A.; Weigel, D.; Herrmann, B.G.  
Cell 67, 79-87, 1991  
A:Title: Expression of a Xenopus homolog of Brachyury (T) is an immediate-early respo  
A:Reference number: A41056; MUID:92005698  
A:Molecule type: mRNA  
A:Residues: 1-432 <SMI>  
A:Cross-references: GB:M77243; NID:g213999; PIDN:AAA49663.1; PID:g214000  
C:Comment: Both basic fibroblast growth factor (bFGF) and activin A induce expression  
C:Genetics:  
A:Gene: Xbra  
C:Superfamily: mouse gene T protein; T-box homology  
C:Keywords: DNA binding; mesoderm; transcription regulation  
F:49-225/Domain: T-box homology <TBX>

Query Match 100.0%; Score 30; DB 1; Length 432;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 121 VYIHP 125

RESULT 11

S08156  
gene T protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S08156  
R:Herrmann, B.G.; Labelit, S.; Poustka, A.; King, T.R.; Lehrach, H.  
Nature 343, 617-622, 1990  
A:Title: Cloning of the T gene required in mesoderm formation in the mouse.  
A:Reference number: S08156; MUID:90158787  
A:Accession: S08156  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-436 <HER>  
A:Cross-references: GB:X51683; NID:g55053; PIDN:CAA35985.1; PID:g55054  
C:Genetics:  
A:Gene: T  
A:Map position: 17  
C:Superfamily: mouse gene T protein; T-box homology  
C:Keywords: DNA binding; transcription regulation  
F:51-227/Domain: T-box homology <TBX>

Query Match 100.0%; Score 30; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||  
Db 123 VYIHP 127

## RESULT 12

T20803  
hypothetical protein F12F6.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T20803  
R:Kershaw, J.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19326  
A:Accession: T20803  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-444 <WIL>  
A:Cross-references: EMBL:273425; PIDN:CAA97789.1; GSPDB:GN00022; CESP:F12F6.3  
A:Experimental source: clone F12F6  
C:Genetics:  
A:Gene: CESP:F12F6.3  
A:Map position: 4  
A:Introns: 27/2; 75/2; 101/2; 161/3; 188/3; 243/3; 284/2; 388/3; 428/3

Query Match 100.0%; Score 30; DB 2; Length 444;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

|||||

Db 47 VYIHP 51

## RESULT 13

JC2318  
angiotensin precursor - sheep  
N:Alternate names: angiotensinogen  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: JC2318; A25406  
R:Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura  
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994  
A:Title: Sequencing and expression of sheep angiotensinogen cDNA.  
A:Reference number: JC2318; MUID:95072318  
A:Accession: JC2318  
A:Molecule type: mRNA  
A:Residues: 1-476 <NAG>  
A:Cross-references: DBJ:DI7520; NID:g575593; PIDN:BAA04470.1; PID:g1197183  
A:Experimental source: liver  
A:Note: the authors translated the codon TTC for residue 465 as Leu  
R:Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.  
Eur. J. Biochem. 154, 597-601, 1986  
A:Title: Purification and characterization of ovine angiotensinogen.  
A:Reference number: A25406; MUID:86136099  
A:Accession: A25406  
A:Molecule type: protein  
A:Residues: 25-37, 'X', 39 <FER>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:24-476/Product: angiotensinogen #status predicted <MPT>  
F:25-34/Product: angiotensin #status predicted <MAT>  
F:295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 30; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

|||||

Db 27 VYIHP 31

## RESULT 14

ANRT

angiotensin precursor - rat  
N:Contents: angiotensin I; angiotensin II; angiotensin III  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 18-Jun-1999  
C:Accession: A93945; A90456; A01251  
R:Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983  
A:Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.  
A:Reference number: A93945; MUID:83169849  
A:Accession: A93945  
A:Molecule type: mRNA  
A:Residues: 1-477 <OHK>  
A:Cross-references: GB:U00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914  
R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.  
Biochemistry 20, 7010-7015, 1981  
A:Title: Rat angiotensinogen and Des(angiotensinI)angiotensinogen: purification, char  
A:Reference number: A90456; MUID:82091819  
A:Accession: A90456  
A:Molecule type: protein  
A:Residues: 25-41 <BOU>  
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted  
e I (angiotensin-converting enzyme), primarily in the lungs.  
C:Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and  
sp-1 angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.  
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.  
ung.  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-477/Product: angiotensinogen #status predicted <MPT>  
F:25-34/Product: angiotensin I #status experimental <BP1>  
F:25-32/Product: angiotensin II #status experimental <PP2>  
F:26-32/Product: angiotensin III #status experimental <PP3>  
F:295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 30; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

|||||

Db 27 VYIHP 31

## RESULT 15

A29978  
angiotensin precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A29978  
R:Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.  
Genomics 2, 240-248, 1988  
A:Title: Molecular cloning of the mouse angiotensinogen gene.  
A:Reference number: A29978; MUID:88284703  
A:Accession: A29978  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-477 <CLO>  
A:Cross-references: GB:AF045887; GB:J03046; NID:g2842773; PIDN:AAC01765.1; PID:g28427  
C:Genetics:  
A:Introns: 277/1; 366/2; 414/3  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-477/Product: angiotensinogen #status predicted <MAT>

Query Match 100.0%; Score 30; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

Db 27 VYHP 31

Search completed: July 1, 2002, 07:46:29  
Job time: 450 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:07 ; Search time 34.05 Seconds  
(without alignments)  
5.686 Million cell updates/sec

Title: US-09-723-197-6  
Perfect score: 30  
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	100.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
2	30	100.0	14	1 ANG2_HORSE	P01016 equus cabal
3	30	100.0	177	1 Y404_TREPA	O83419 treponema p
4	30	100.0	378	1 EXT1_CAEEL	O01704 caenorhabdi
5	30	100.0	397	1 T8XT_CHICK	P79778 gallus gall
6	30	100.0	423	1 BRAC_BRARE	Q07998 brachydanio
7	30	100.0	432	1 BRAC_XENLA	P24781 xenopus lae
8	30	100.0	433	1 BRAC_CHICK	P79777 gallus gall
9	30	100.0	435	1 BRAC_HUMAN	O15178 homo sapien
10	30	100.0	436	1 BRAC_MOUSE	P20293 mus musculu
11	30	100.0	436	1 TBX6_HUMAN	O95947 homo sapien
12	30	100.0	440	1 BRA2_BRAFL	P80492 branchiosto
13	30	100.0	448	1 BRA1_BRAFL	Q17134 branchiosto
14	30	100.0	448	1 TX19_HUMAN	O60806 homo sapien
15	30	100.0	476	1 ANG2_SHEEP	P20757 ovis aries
16	30	100.0	477	1 ANG2_MOUSE	P11859 mus musculu
17	30	100.0	477	1 ANG2_RAT	P01015 rattus norv
18	30	100.0	485	1 ANG2_HUMAN	P01019 homo sapien
19	30	100.0	501	1 TX18_HUMAN	O95935 homo sapien
20	30	100.0	540	1 TBX6_MOUSE	P70327 mus musculu
21	30	100.0	602	1 TX15_MOUSE	O70306 mus musculu
22	30	100.0	613	1 TX18_MOUSE	Q9epz6 mus musculu
23	30	100.0	678	1 SIK1_YEAST	P21691 saccharomyc
24	30	100.0	980	1 SYV_SCHPO	O75005 schizosacch
25	30	100.0	1055	1 CC28_SCHPO	Q10752 schizosacch
26	30	100.0	1121	1 DX8_ARATH	O38953 arabidopsis
27	30	100.0	1200	1 DX8_CAEEL	O09530 caenorhabdi
28	30	100.0	1220	1 DX8_HUMAN	Q14562 homo sapien
29	30	100.0	1267	1 DRI1_YEAST	Q04217 saccharomyc
30	30	100.0	1355	1 VG46_HSV11	Q00104 ictaluriid h
31	29	96.7	10	1 ANG1_BOTJA	P010581 bothrops ja
32	29	96.7	10	1 ANG2_BOVIN	P01017 bos taurus
33	29	96.7	10	1 ANG2_CHICK	P01018 gallus gall

34	29	96.7	172	1 YNCA_ECOLI	P76112 escherichia
35	29	96.7	288	1 GIL2_ENTHI	Q03077 entamoeba h
36	29	96.7	391	1 PYRC_USTWA	P31301 ustilago ma
37	29	96.7	471	1 BRAC_HALRO	P56158 halocynthia
38	29	96.7	528	1 GD_DROME	O62589 drosophila
39	29	96.7	617	1 THRB_RAT	P18292 rattus norv
40	29	96.7	622	1 THRB_HUMAN	P00734 homo sapien
41	29	96.7	625	1 THRB_BOVIN	P00735 bos taurus
42	29	96.7	692	1 EOWD_XENLA	P79944 xenopus lae
43	29	96.7	702	1 CRN_DROME	P17886 drosophila
44	28	93.3	11	1 ANG2_CRIGE	P09037 crinia geor
45	28	93.3	144	1 SALT_ORYSA	P24120 oryza sativ

ALIGNMENTS

RESULT 1					
ID	ANG2_BOTJA	STANDARD;	PRT;	8 AA.	
AC	Q10582;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	Angiotensin-like peptide II (Fragment).				
OS	Bothrops jararaca (Jararaca).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;				
OC	Viperidae; Crotalinae; Bothrops.				
OX	NCBI_TaxID=8724;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Plasma;				
RX	MEDLINE=96208932; PubMed=8829801;				
RA	Borgheresi R.A.M.B., Dalle Luca J., Carmona E., Picarelli Z.P.;				
RT	"Isolation and identification of angiotensin-like peptides from the				
RT	plasma of the snake Bothrops jararaca."				
RL	Comp. Biochem. Physiol. 113B:467-473(1996).				
CC	-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.				
DR	InterPro; IPR000215; Serpin.				
DR	PROSITE; PS00284; SERPIN; PARTIAL.				
KW	Vasoconstrictor; Plasma; Serpin.				
FT	NON_TER 8				
SQ	SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;				

Query Match 100.0%; Score 30; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 VYIHP 5
DB	3 VYIHP 7

RESULT 2					
ID	ANG2_HORSE	STANDARD;	PRT;	14 AA.	
AC	P01016;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).				
GN	SERPINA8 OR AGT.				
OS	Equus caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
OX	NCBI_TaxID=9796;				
RN	[1]				
RP	SEQUENCE.				
RA	Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;				
RT	"The preparation, purification, and amino acid sequence of a				
RT	polypeptide renin substrate."				

RL J. Exp. Med. 106:439-453(1957).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR; A01250; A01250.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBD7 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 3 VYIHP 7

RESULT 3  
Y404\_TREPA STANDARD; PRT; 177 AA.  
AC 083419;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein TP0404.

GN TP0404.  
OS Treponema pallidum.  
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=160;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NICHOLS;  
RX MEDLINE=98332770; PubMed=9665876;  
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,  
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,  
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,  
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,  
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,  
RA Venter J.C.;  
RA "Complete genome sequence of Treponema pallidum, the syphilis  
RT spirochete";  
RL Science 281:375-388(1998).

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CC -----  
CC EMBL; AE001218; AAC65395.1; -  
DR TIGR; TP0404; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 177 AA; 19491 MW; A9395B74FA052F93 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 3 VYIHP 7

RESULT 4  
EXTL\_CAEEL STANDARD; PRT; 378 AA.  
ID EXTL\_CAEEL  
AC 001704;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Multiple exostoses homolog 1.  
GN RIB-1.  
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=97264342; PubMed=9110175;  
RA Clines G.A., Ashley J.A., Shah S., Lovett M.;  
RT "The structure of the human multiple exostoses 2 gene and  
RT characterization of homologs in mouse and Caenorhabditis elegans.";  
RL Genome Res. 7:359-367(1997).  
CC -1- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.  
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CC -----  
DR EMBL; U94834; AAC47509.1; -  
SQ SEQUENCE 378 AA; 44453 MW; 5CE6ECF3AA89647E CRC64;

Query Match 100.0%; Score 30; DB 1; Length 378;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 43 VYIHP 47

RESULT 5  
TBXT\_CHICK STANDARD; PRT; 397 AA.  
ID TBXT\_CHICK  
AC P79778;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box containing protein TBXT.  
GN TBXT.  
OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=WHITE LECHORN; TISSUE=Embryo;  
RX MEDLINE=97178976; PubMed=9053317;  
RA Knezevic V., de Santo R., Macken S.;  
RT "Two novel chick T-box genes related to mouse Brachyury are expressed  
RT in different, non-overlapping mesodermal domains during  
RT gastrulation.";  
RL Development 124:411-419(1997).  
CC -1- FUNCTION: MAY BE INVOLVED IN THE INITIAL FORMATION OF THE  
CC CHORDAMESODERM.

CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED IN THE EARLY PRIMITIVE  
 CC STREAK. BY STAGE 4, IN HENSEN'S NODE, EARLY PRECHORDAL PLATE AND  
 CC NOTOCHORD. ALSO EXPRESSED IN EARLY DEVELOPMENT IN THE NEURAL  
 CC PLATE ECTODERM IMMEDIATELY ANTERIOR TO HENSEN'S NODE. EXPRESSION  
 CC NOT DETECTED AFTER STAGE 10-12.  
 CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
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 CC EMBL; U67087; AAC60072.1; -  
 CC HSSP; P24781; 1XBR.  
 CC InterPro; IPR001699; T-box.  
 CC Pfam; PF00907; T-box; 1.  
 CC PRINTS; PR00937; TBOX.  
 CC SMART; SM00425; TBOX; 1.  
 CC PROSITE; PS01283; TBOX\_1; 1.  
 CC PROSITE; PS01264; TBOX\_2; 1.  
 CC PROSITE; PS02522; TBOX\_3; 1.  
 CC Developmental protein; Transcription regulation; DNA-binding;  
 KW Nuclear protein.  
 FT DNA\_BIND 48 216 T-BOX  
 FT SEQUENCE 397 AA; 43686 MW; 8F137C7D271D393B CRC64;

Query Match 100.0%; Score 30; DB 1; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
 |||||  
 DB 120 VYIHP 124

RESULT 6  
 BRAC\_BRARE STANDARD; PRT; 423 AA.  
 ID BRAC\_BRARE  
 AC Q07998;  
 DT 01-NOV-1997 (Rel. 35; Created)  
 DT 01-NOV-1997 (Rel. 35; Last sequence update)  
 DT 01-MAR-2002 (Rel. 41; Last annotation update)  
 DE Brachyury protein homolog (T-box protein homolog) (T-box protein 2FT) (2F-  
 T).  
 GN T OR NTL.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93201989; PubMed=1295726;  
 RA Schulte-Merker S., Ho R.K., Herrmann B.G., Nusslein-Volhard C.;  
 RT "The protein product of the zebrafish homologue of the mouse T gene  
 RT is expressed in nuclei of the germ ring and the notochord of the  
 RT early embryo."  
 RL Development 116:1021-1032(1992).  
 CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES  
 CC REQUIRED FOR MESODERM DIFFERENTIATION (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- TISSUE SPECIFICITY: EARLY EMBRYO. HIGHEST LEVELS FOUND AT ALL  
 CC STAGES IN DEVELOPING NOTOCHORD. ALSO FOUND, BEFORE GASTRULATION,  
 CC IN THE PRESUMPTIVE MESODERM AND ENDODERM (THE GERM RING) AS WELL  
 CC AS IN ENVELOPING CELLS.  
 CC -!- DEVELOPMENTAL STAGE: IN DEVELOPING EMBRYO, FIRST EXPRESSED IN THE  
 CC DOMING STAGE (4.2 HOURS). HIGHEST EXPRESSION FOUND BETWEEN 5.2 AND

CC 9.5 HOURS (EPIBOLY) AFTER WHICH, LEVELS GRADUALLY DECREASE AND BY  
 CC 48 HOURS, NO MORE EXPRESSION IS OBSERVED.  
 CC -!- INDUCTION: BY MESODERM-INDUCING FACTOR ACTIVIN A.  
 CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL; S57147; AAB25829.1; -  
 CC HSSP; P24781; 1XBR.  
 CC ZFIN; ZDB-GENE-980526-437; ntl.  
 CC InterPro; IPR001699; T-box.  
 CC Pfam; PF00907; T-box; 1.  
 CC PRINTS; PR00937; TBOX.  
 CC SMART; SM00425; TBOX; 1.  
 CC PROSITE; PS01283; TBOX\_1; 1.  
 CC PROSITE; PS01264; TBOX\_2; 1.  
 CC PROSITE; PS02522; TBOX\_3; 1.  
 CC Developmental protein; Transcription regulation; DNA-binding;  
 KW Nuclear protein; Activator.  
 FT DNA\_BIND 44 212 T-BOX  
 FT SEQUENCE 423 AA; 45834 MW; 96FEB8109EF4407E CRC64;

Query Match 100.0%; Score 30; DB 1; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
 |||||  
 DB 116 VYIHP 120

RESULT 7  
 BRAC\_XENLA STANDARD; PRT; 432 AA.  
 ID BRAC\_XENLA  
 AC P24781;  
 DT 01-MAR-1992 (Rel. 21; Created)  
 DT 01-MAR-1992 (Rel. 21; Last sequence update)  
 DT 01-MAR-2002 (Rel. 41; Last annotation update)  
 DE Brachyury protein (T protein) (XBRA).  
 GN BRA.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92005698; PubMed=1717160;  
 RA Smith J.C., Price B.M., Green J.B., Weigel D., Herrmann B.G.;  
 RT "Expression of a xenopus homolog of Brachyury (T) is an immediate-  
 RT early response to mesoderm induction."  
 RL Cell 67:79-87(1991).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=94147980; PubMed=7906224;  
 RA Cunliffe V., Smith J.C.;  
 RT "Specification of mesodermal pattern in Xenopus laevis by  
 RT interactions between Brachyury, noggin and Xwnt-8."  
 RL EMBO J. 13:349-359(1994).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 39-222.  
 RX MEDLINE=98007980; PubMed=9349824;  
 RA Mueller C.W., Herrmann B.G.;  
 RT "Crystallographic structure of the T domain-DNA complex of the  
 RT Brachyury transcription factor."  
 RL Nature 389:884-888(1997).

CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES  
CC REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. CAUSES DORSAL  
CC MESODERMAL DIFFERENTIATION OF ANIMAL CAP ECTODERM WHEN CO-  
CC EXPRESSED WITH XWNT-8 AND NOGGIN. NONE OF THESE MOLECULES CAUSES  
CC DORSAL MESODERM FORMATION WHEN EXPRESSED ALONE.  
CC -!- SUBUNIT: MONOMER.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PRESUMPTIVE MESODERMAL CELLS  
CC AROUND THE BLASTOPORE, AND THEN IN THE NOTOCHORD.  
CC -!- DEVELOPMENTAL STAGE: DURING GASTRULA AND NEURULA STAGES IN  
CC INVOLUTING MESODERM AND IN THE NOTOCHORD.  
CC -!- INDUCTION: BY THE NATURAL SIGNAL AND IN RESPONSE TO THE MESODERM-  
CC INDUCING FACTORS ACTIVIN A AND BASIC FGF.  
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
CC  
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CC  
CC EMBL; M77243; AAA49663.1; -  
CC PIR; A41056; A41056.  
CC PDB; 1XBR; 14-JAN-98.  
CC InterPro: IPR001699; T-box.  
CC Pfam; PF00907; T-box; 1.  
CC PRINTS; PR00937; TBOX.  
CC SMART; SM00425; TBOX; 1.  
CC PROSITE; PS01283; TBOX\_1; 1.  
CC PROSITE; PS01264; TBOX\_2; 1.  
CC PROSITE; PS50252; TBOX\_3; 1.  
CC DEVELOPMENTAL protein; Transcription regulation; DNA-binding;  
CC Nuclear protein; Activator; 3D-structure.  
FT DNA\_BIND 49 217 T-BOX.  
SQ SEQUENCE 432 AA; 47599 MW; 2F91D942D86EE60A CRC64;  
  
Query Match 100.0%; Score 30; DB 1; Length 432;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VYIHP 5  
Db 121 VYIHP 125  
|||||  
  
RESULT 8  
BRAC\_CHICK STANDARD; PRT; 433 AA.  
AC P79777; Q90654;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Brachyury protein (T protein).  
GN T.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OC NCBI\_TaxID=9031;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Embryo;  
RX MEDLINE=95246917; PubMed=7729577;  
RA Kispert A., Orthen H., Cooke J., Herrmann B.G.;  
RT "The chick brachyury gene: developmental expression pattern and  
RT response to axial induction by localized activin.";  
RL Dev. Biol. 168:406-415(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WHITE LEHORN; TISSUE=Embryo;

RX MEDLINE=97178976; PubMed=9053317;  
RA Knezevic V., de Santo R., Mackem S.;  
RT "Two novel chick T-box genes related to mouse Brachyury are expressed  
RT in different, non-overlapping mesodermal domains during  
RT gastrulation.";  
RL Development 124:411-419(1997).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Heart;  
RA Huang J.X., Wendler C.C., Morrice D.R., Burt D.W., Runyan R.B.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES  
CC REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. BINDS TO A  
CC PALINDROMIC SITE (CALLED T SITE) AND ACTIVATES GENE TRANSCRIPTION  
CC WHEN BOUND TO SUCH A SITE (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED IN THE POSTERIOR EPIBLAST OF  
CC STAGE XII BLASTODERM, THEN IN THE ELONGATING PRIMITIVE STREAK,  
CC EARLY MIGRATING MESODERM, HENSEN'S NODE AND IN THE NOTOCHORD.  
CC IN LATER STAGES, FOUND IN TAIL BUD AND ENTIRE NOTOCHORD UP TO  
CC STAGE 26-28.  
CC -!- INDUCTION: BY FGF-4 AND ACTIVIN.  
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
CC  
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CC  
CC EMBL; U67086; AAC60283.1; -  
CC EMBL; U25176; AAA67365.1; -  
CC HSP; P24781; IXBR.  
CC InterPro: IPR001699; T-box.  
CC Pfam; PF00907; T-box; 1.  
CC PRINTS; PR00937; TBOX.  
CC SMART; SM00425; TBOX; 1.  
CC PROSITE; PS01283; TBOX\_1; 1.  
CC PROSITE; PS01264; TBOX\_2; 1.  
CC PROSITE; PS50252; TBOX\_3; 1.  
CC DEVELOPMENTAL protein; Transcription regulation; DNA-binding;  
CC Nuclear protein; Activator.  
FT DNA\_BIND 49 217 T-BOX.  
FT CONFLICT 250 250 A -> T (IN REF. 3).  
SQ SEQUENCE 433 AA; 47289 MW; 8C0C27577E92872F CRC64;  
  
Query Match 100.0%; Score 30; DB 1; Length 433;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VYIHP 5  
Db 121 VYIHP 125  
|||||  
  
RESULT 9  
BRAC\_HUMAN STANDARD; PRT; 435 AA.  
ID BRAC\_HUMAN  
AC O15178;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Brachyury protein (T protein).  
GN T.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP

RX MEDLINE=96402060; PubMed=8963900;  
RA Edwards Y.H., Putt W., Lekoape K.M., Stott D., Fox M., Hopkinson D.A.,  
RA Sowden J.;  
RT "The human homolog T of the mouse T(Brachyury) gene; gene structure,  
RT cDNA sequence, and assignment to chromosome 6q27.";  
RL Genome Res. 6:226-233(1996).  
CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES  
CC REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. BINDS TO A  
CC PALINDROMIC SITE (CALLED T SITE) AND ACTIVATES GENE TRANSCRIPTION  
CC WHEN BOUND TO SUCH A SITE.  
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
CC -----  
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CC -----  
DR EMBL; AJ001699; CAA04938.1; -  
DR HSSP; P24781; 1XBR.  
DR MIM; 601397; -  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
KW Developmental protein; Transcription regulation; DNA-binding;  
KW Nuclear protein; Activator.  
FT DNA\_BIND 51 219 T-BOX.  
SQ SEQUENCE 435 AA; 47443 MW; 9D470088C8602631 CRC64;  
  
Query Match 100.0%; Score 30; DB 1; Length 435;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VVIHP 5  
| | | | |  
Db 123 VVIHP 127  
  
RESULT 10  
BRAC\_MOUSE  
ID BRAC\_MOUSE STANDARD; PRT; 436 AA.  
AC P20293;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Brachyury protein (T protein).  
GN T.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9015878; PubMed=2154694;  
RA Herrmann B.G., Labelt S., Poustka A., King T.R., Lehrach H.;  
RT "Cloning of the T gene required in mesoderm formation in the mouse."  
RL Nature 343:617-622(1990).  
RN [2]  
RP CHARACTERIZATION.  
RX MEDLINE=93345466; PubMed=8344258;  
RA Kispert A., Herrmann B.G.;  
RT "The Brachyury gene encodes a novel DNA binding protein.";  
RL EMO J. 12:3211-3220(1993).  
RN [3]

RP CHARACTERIZATION.  
RX MEDLINE=96030782; PubMed=7588606;  
RA Kispert A., Koschorz B., Herrmann B.G.;  
RT "The T protein encoded by Brachyury is a tissue-specific  
RT transcription factor.";  
RL EMO J. 14:4763-4772(1995).  
CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES  
CC REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. BINDS TO A  
CC PALINDROMIC SITE (CALLED T SITE) AND ACTIVATES GENE TRANSCRIPTION  
CC WHEN BOUND TO SUCH A SITE.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DEVELOPMENTAL STAGE: DURING GASTRULA AND NEURULA STAGES IN  
CC INVOLUTING MESODERM AND IN THE NOTOCHORD.  
CC -!- DISEASE: EMBRYO LACKING THE T GENE FAIL TO FORM THE NOTOCHORD.  
CC THE ENTIRE POSTERIOR REGION AND THE ALLANTOIS, AND DIE AT ABOUT  
CC 10 DAYS OF GESTATION.  
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
CC -----  
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CC -----  
DR EMBL; X51683; CAA35985.1; -  
DR PIR; S08156; S08156.  
DR HSSP; P24781; 1XBR.  
DR TRANSFAC; T01526; -  
DR MGD; MGI:98472; T.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
KW Developmental protein; Transcription regulation; DNA-binding;  
KW Nuclear protein; Activator.  
FT DNA\_BIND 51 219 T-BOX.  
SQ SEQUENCE 436 AA; 47440 MW; 1A0BDF9BA7FC2484 CRC64;  
  
Query Match 100.0%; Score 30; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VVIHP 5  
| | | | |  
Db 123 VVIHP 127  
  
RESULT 11  
TEX6\_HUMAN  
ID TEX6\_HUMAN STANDARD; PRT; 436 AA.  
AC O95947;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX6 (T-box protein 6).  
GN TBX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99134303; PubMed=99333572;  
RA Papapetrou C., Putt W., Fox M., Edwards Y.H.;  
RT "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";  
RL Genomics 55:238-241(1999).

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RN RP SEQUENCE OF 135-272 FROM N.A.
RC TISSUE=Myeloid;
RA Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA Anström-Buissert L., McClure P., Slingsby T., Brook J.D.;
RT "Identification, mapping and phylogenomic analysis of four new human
RT members of the T-box gene family: EOMES, TBX6, TBX16, and TBX19."
RL Genomics 55:10-20(1999).
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
CC PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
CC TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
CC TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
CC SECOND PHASE IN SOME ADULT TISSUES.
CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC -----
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CC -----
DR EMBL; AJ007989; CAA07812.1; -.
DR EMBL; AJ010279; CAB37938.1; -.
DR HSSP; P24781; 1XBR.
DR TM: 602427; -.
DR InterPro: IPR001699; T-box.
DR Pfam: PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
DR Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein.
FT DNA_BIND 100 273 T-BOX.
FT CONFLICT 207 207 H -> HV (IN REF. 2).
FT SEQUENCE 436 AA; 47017 MW; 438178BD31B966E9 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5
DB 172 VYIHP 176
|||||

RESULT 12
BRA2_BRAFL
ID BRA2_BRAFL STANDARD; PRT; 440 AA.
AC P80492;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Brachyury protein homolog 2 (AmBra-2).
GN BRA-2.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96125169; PubMed=8575328;
RA Holland P.W.H., Koschorz B., Holland L.Z., Herrmann B.G.;
RT "Conservation of Brachyury (T) genes in amphioxus and vertebrates:
RT developmental and evolutionary implications."
RL Development 121:4283-4291(1995).
CC -1- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE 10 H GASTRULA AROUND
CC THE BLASTOPORE. IN LATER STAGES OF GASTRULATION AND EARLY
CC NEURALIZATION, EXPRESSED IN POSTERIOR MESODERM AND THE NOTOCHORD
CC WHERE EXPRESSION CONTINUES AT LEAST UNTIL SWIMMING LARVAL STAGE.
CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC -----
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CC -----
DR EMBL; X91903; CAA62999.1; -.
DR HSSP; P24781; 1XBR.

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RT "Conservation of Brachyury (T) genes in amphioxus and vertebrates:
RT developmental and evolutionary implications."
RL Development 121:4283-4291(1995).
CC -1- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: MESODERM AND NOTOCHORD.
CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
HSSP: P24781; 1XBR.
DR InterPro: IPR001699; T-box.
DR Pfam: PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
KW Developmental protein; Transcription regulation; DNA-binding;
FT Nuclear protein; Multigene family.
FT DNA_BIND 44 215 T-BOX.
FT SEQUENCE 440 AA; 48469 MW; F12EBC417243D3D6 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 440;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5
DB 116 VYIHP 120
|||||

RESULT 13
BRAL_BRAFL
ID BRAL_BRAFL STANDARD; PRT; 448 AA.
AC Q17134;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Brachyury protein homolog 1 (AmBra-1).
GN BRA-1.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Larva;
RX MEDLINE=96125169; PubMed=8575328;
RA Holland P.W.H., Koschorz B., Holland L.Z., Herrmann B.G.;
RT "Conservation of Brachyury (T) genes in amphioxus and vertebrates:
RT developmental and evolutionary implications."
RL Development 121:4283-4291(1995).
CC -1- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE 10 H GASTRULA AROUND
CC THE BLASTOPORE. IN LATER STAGES OF GASTRULATION AND EARLY
CC NEURALIZATION, EXPRESSED IN POSTERIOR MESODERM AND THE NOTOCHORD
CC WHERE EXPRESSION CONTINUES AT LEAST UNTIL SWIMMING LARVAL STAGE.
CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X91903; CAA62999.1; -.
DR HSSP; P24781; 1XBR.

```

DR InterPro; IPR001699; T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01283; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS0252; TBOX\_3; 1.  
 KW Developmental protein; Transcription regulation; DNA-binding;  
 KW Nuclear protein; Multigene family.  
 FT DNA\_BIND 54 224  
 T-BOX.  
 SQ SEQUENCE 448 AA; 49253 MW; 43326D32FD4BC156 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
 |||||  
 Db 126 VYIHP 130

## RESULT 14

TX19\_HUMAN STANDARD; PRT; 448 AA.  
 AC O60806;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE T-box transcription factor TBX19 (T-box protein 19).  
 GN TBX19.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;

FN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99107806; PubMed=9888994;

RA Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,  
 RA Anström-Buisseret L., McClure P., Slingsby T., Brook J.D.;  
 RT Identification, mapping and phylogenomic analysis of four new human  
 RT members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";  
 RL Genomics 55:10-20(1999).  
 RN [2]

RP SEQUENCE OF 3-437 FROM N.A.

RA Wray P.;

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN  
 CC DEVELOPMENTAL PROCESSES.

CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

CC -----  
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CC -----  
 CC EMBL; AJ010277; CAB37936.1; -.  
 CC EMBL; AL009051; CAA15624.1; -.  
 CC HSSP; P24781.1XBR.  
 CC MIN; 604614; -.

DR InterPro; IPR001699; T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01283; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS0252; TBOX\_3; 1.

KW Transcription regulation; DNA-binding; Nuclear protein.  
 FT DNA\_BIND 50 218  
 T-BOX.

SQ SEQUENCE 448 AA; 48238 MW; B7B1DFF14B8B53C5 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
 |||||  
 Db 122 VYIHP 126

## RESULT 15

ANGT\_SHEEP STANDARD; PRT; 476 AA.  
 AC P20757;

DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
 GN SERPIN A8 OR AGT.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID=9940;

FN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=95072318; PubMed=7765514;

RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,

RA Murakami K., Nakamura Y.;

RT "Sequencing and expression of sheep angiotensinogen cDNA.";  
 RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).  
 RN [2]

RP SEQUENCE OF 25-39.

RX MEDLINE=86136099; PubMed=3081342;

RA Fernley R.T., John M., Niall H.D., Coghlan J.P.;

RT "Purification and characterization of ovine angiotensinogen.";  
 RL Eur. J. Biochem. 154:597-601(1986).

CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.

CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

CC -----  
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CC -----  
 CC EMBL; D17520; BAA04470.1; -.  
 CC PIR; A25406; A25406.

DR InterPro; IPR000227; Angiotensngn.

DR InterPro; IPR000215; Serpin.

DR Pfam; PF000079; serpin; 1.

DR PRINTS; PR00654; ANGIOTENSGN.

DR SMART; SM00093; SERPIN; 1.

DR PROSITE; PS00284; SERPIN; 1.

KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.

FT SIGNAL 1 24

FT CHAIN 25 476 ANGIOTENSINOGEN.

FT PEPTIDE 25 34 ANGIOTENSIN I.

FT PEPTIDE 25 32 ANGIOTENSIN II.

FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
| | | | |  
Db 27 VYIHP 31

Search completed: July 1, 2002, 07:47:08  
Job time: 474 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:11 ; Search time 122.73 seconds  
(without alignments)  
7.048 Million cell updates/sec

Title: US-09-723-197-6

Perfect score: 30

Sequence: 1 VYIHP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_l9:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	100.0	14	5 Q10757	Q10757 theromyzon
2	30	100.0	63	6 Q95KV3	Q95kv3 bos taurus
3	30	100.0	101	12 Q9EN21	Q9en21 amsacta moo
4	30	100.0	124	16 Q98AY8	Q98ay8 rhizobium l
5	30	100.0	130	13 P79705	P79705 cynops pyrr
6	30	100.0	171	17 Q97IG2	Q97ig2 sulfolobus
7	30	100.0	183	5 Q9N866	Q9n866 leishmania
8	30	100.0	184	4 Q75406	Q75406 homo sapien
9	30	100.0	184	16 Q92CGO	Q92cgo listeria in
10	30	100.0	245	6 Q95J13	Q95j13 pan troglod
11	30	100.0	265	5 Q9XYF5	Q9xyf5 hydra atten
12	30	100.0	295	4 Q9HA44	Q9ha44 homo sapien
13	30	100.0	295	5 Q96040	Q96040 ptychodera
14	30	100.0	317	11 Q923Q5	Q923q5 mus musculus
15	30	100.0	323	5 Q9VZ11	Q9vz11 drosophila
16	30	100.0	344	13 Q98SM4	Q98sm4 eleutheroda

17	30	100.0	382	5 Q9U3J6	Q9u3j6 caenorhabdi
18	30	100.0	385	10 Q9SJ94	Q9sj94 arabisdopsis
19	30	100.0	399	4 Q9Y5P5	Q9y5p5 homo sapien
20	30	100.0	402	5 Q95WL2	Q95wl2 hydractinia
21	30	100.0	411	10 Q9SSG7	Q9ssg7 arabisdopsis
22	30	100.0	415	10 Q9C9P3	Q9c9p3 arabisdopsis
23	30	100.0	418	13 Q90ZA4	Q90za4 ambystoma m
24	30	100.0	419	10 Q9FQ10	Q9fq10 medicago tr
25	30	100.0	419	13 Q42100	Q42100 oryzias lat
26	30	100.0	420	4 Q9NWC3	Q9nwc3 homo sapien
27	30	100.0	420	4 Q961J6	Q961j6 homo sapien
28	30	100.0	420	11 Q922H4	Q922h4 mus musculu
29	30	100.0	434	13 Q9W7R8	Q9w7r8 xenopus lae
30	30	100.0	435	6 Q9GL27	Q9gl27 canis famil
31	30	100.0	436	11 Q9CSJ0	Q9csj0 mus musculu
32	30	100.0	439	13 Q57386	Q57386 cynops pyrr
33	30	100.0	442	5 Q9GNV1	Q9gnv1 platynereis
34	30	100.0	446	11 Q99ME7	Q99me7 mus musculu
35	30	100.0	449	4 Q9BVA6	Q9bva6 homo sapien
36	30	100.0	461	11 Q9D2V0	Q9d2v0 mus musculu
37	30	100.0	477	4 Q96FD5	Q96fd5 homo sapien
38	30	100.0	485	4 Q96F91	Q96f91 homo sapien
39	30	100.0	485	6 Q9GLP7	Q9glp7 pan troglod
40	30	100.0	485	6 Q9GLP6	Q9glp6 gorilla gor
41	30	100.0	485	6 Q9GLN8	Q9gln8 pan troglod
42	30	100.0	486	6 Q9TSZ0	Q9tsz0 callithrix
43	30	100.0	513	10 Q9LWF6	Q9lwf6 oryza sativ
44	30	100.0	533	4 Q96SF7	Q96sf7 homo sapien
45	30	100.0	695	5 Q9XUQ0	Q9xuq0 caenorhabdi

## ALIGNMENTS

RESULT 1

Q10757 PRELIMINARY; PRT; 14 AA.  
ID Q10757  
AC Q10757;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE ANGIOTENSINOGEN (FRAGMENT).  
OS Theromyzon tessulatum (Leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
RX NCBI\_TaxID=13286;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95365039; PubMed=7637887;  
RA Laurent V., Bulet P., Salzet M.A.;  
RT 'A comparison of the leech Theromyzon tessulatum angiotensin I-like  
RT molecule with forms of vertebrate angiotensinogens: a hormonal system  
RT conserved in the course of evolution.';  
RL Neurosci. Lett. 190:175-178(1995).  
RN [2]  
RP SEQUENCE OF 1-10.  
RC TISSUE=BRAIN;  
RX MEDLINE=96201949; PubMed=8612806;  
RA Laurent V., Salzet M.;  
RT 'Metabolism of angiotensins by head membranes of the leech Theromyzon  
RT tessulatum.';  
RL FEBS Lett. 384:123-127(1996).  
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.  
KW Glycoprotein; Serpin.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEFBD7 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5

Db 3 VYIHP 7  
|||||

RESULT 2  
Q95KV3 ID Q95KV3 PRELIMINARY; PRT; 63 AA.  
AC Q95KV3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE BRACHYURY PROTEIN (FRAGMENT).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA de Wit A.A.C., Boerjan M.L., Kruij T.A.M.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ13216; CAC88365.1; -;  
FT NON\_TER 1  
FT NON\_TER 63  
SQ SEQUENCE 63 AA; 7130 MW; 67B9163720413171 CRC64;

Query Match 100.0%; Score 30; DB 6; Length 63;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 58 VYIHP 62  
|||||

RESULT 3  
Q9EN21 ID Q9EN21 PRELIMINARY; PRT; 101 AA.  
AC Q9EN21;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE AMV027.  
GN AMV027.  
OS Anascta moorei entomopoxvirus (AmEPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
OC Entomopoxvirus B.  
OX NCBI\_TaxID=28321;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bowden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,  
RA Moyer R.W.;  
RX MEDLINE=20396580; PubMed=10936094;  
RT "Complete Genomic Sequence of the Anascta moorei Entomopoxvirus:  
RT Analysis and Comparison with Other Poxviruses.";  
RL Virology 274:120-139(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bowden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,  
RA Moyer R.W.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF250284; AAG02733.1; -;  
SQ SEQUENCE 101 AA; 12286 MW; 7ECA507CD63762CC CRC64;

Query Match 100.0%; Score 30; DB 12; Length 101;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 76 VYIHP 80  
|||||

RESULT 4  
Q98AY8 ID Q98AY8 PRELIMINARY; PRT; 124 AA.  
AC Q98AY8;  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE MLL5800 PROTEIN.  
GN MLL5800.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAFF303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti.";  
RL DNA Res. 7:331-338(2000).  
DR EMBL; AP003007; BAB52184.1; -;  
KW Complete proteome.  
SQ SEQUENCE 124 AA; 13781 MW; F1280829A42DD9A2 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 124;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
Db 51 VYIHP 55  
|||||

RESULT 5  
P79705 ID P79705 PRELIMINARY; PRT; 130 AA.  
AC P79705;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE BRACHURY (FRAGMENT).  
OS Cynops pyrrhogaster (Japanese common newt).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.  
OX NCBI\_TaxID=8330;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=EMBRYO;  
RA Suzuki A.S., Tabata T., Sakaguchi K., Takabatake T., Takeshima K.,  
RA Kaneda T.;  
RT "Serial expression of the genes in a mesodermizing ectoderms of  
RT early Cynops gastrula.";  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; D89442; BAA13957.1; -;  
DR HSSP; P24781; IXHR.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS50252; TBOX\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 130  
SQ SEQUENCE 130 AA; 14671 MW; B1A834C01890D025 CRC64;

Query Match 100.0%; Score 30; DB 13; Length 130;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
Db 61 VYIHP 65

RESULT 6  
ID Q971G2 PRELIMINARY; PRT; 171 AA.  
AC Q971G2;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE HYPOTHETICAL PROTEIN ST1391.  
GN ST1391.  
OS Sulfolobus tokodaii.  
OC Archaea: Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
OX NCBI\_TaxID=111955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JCM 10545 / 7;  
RX PubMed=11572479;  
RA Kavarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,  
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
RA Oshima T., Kikuchi H.;  
RT "Complete genome sequence of an aerobic thermophilic  
RT Crenarchaeon, Sulfolobus tokodaii strain7.";  
RL DNA Res. 8:123-140(2001).  
DR EMBL; AP000986; BAB66458.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 171 AA; 18700 MW; 897F357EAD34EFOA CRC64;

Query Match 100.0%; Score 30; DB 17; Length 171;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
Db 18 VYIHP 22

RESULT 7  
ID Q9N866 PRELIMINARY; PRT; 183 AA.  
AC Q9N866;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE.  
GN L8382.11.  
OS Leishmania major.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FRIEDLIN;  
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL365476; CAB97039.1; -.  
KW Helicase.  
SQ SEQUENCE 183 AA; 20551 MW; BEE0ED6545831F85 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 183;  
Best Local Similarity 100.0%; Pred. No. 88;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VYIHP 5  
Db 129 VYIHP 133

RESULT 8  
ID Q75406 PRELIMINARY; PRT; 184 AA.  
AC Q75406;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE HUNTINGTIN INTERACTING PROTEIN HYPE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=FRONTAL CORTEX;  
RA Faber P.W., Barnes G.T., Srinidhi J., Chen J., Gusella J.F.,  
RA MacDonald M.E.;  
RT "Huntingtin interacts with a family of WW domain proteins.";  
RL Hum. Mol. Genet. 0:0-0(1998).  
DR EMBL; AF049611; AAC26847.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 184 AA; 20919 MW; 5FB5DE1093D99B20 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5  
Db 86 VYIHP 90

RESULT 9  
ID Q92CG0 PRELIMINARY; PRT; 184 AA.  
AC Q92CG0;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE LIN1212 PROTEIN.  
GN LIN1212.  
OS Listeria innocua.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1642;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIP 11262 / SEROVAR 6A;  
RX PubMed=11679669;  
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,  
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,  
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,  
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,  
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,  
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,  
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;  
RT "Comparative genomics of Listeria species.";  
RL Science 294:849-852(2001).  
DR EMBL; AL596168; CAC96443.1; -.  
DR Listlist; LIN01212; -.  
KW Complete proteome.

SQ SEQUENCE 184 AA; 21570 MW; 5A842734193A7F66 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 184;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
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Db 92 VYIHP 96

RESULT 10

Q95J13 ID Q95J13 PRELIMINARY; PRT; 245 AA.  
AC Q95J13;  
DT 01-DEC-2001 (TEMBLrel. 19, Created)  
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN (FRAGMENT).  
GN REN.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=504, AND 505;  
RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB062027; BAB55856.1; -;  
DR EMBL; AB062028; BAB55857.1; -;  
FT NON\_TER 245 245  
SQ SEQUENCE 245 AA; 26317 MW; E0092390B99803E0B CRC64;

Query Match 100.0%; Score 30; DB 6; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||

Db 36 VYIHP 40

RESULT 11

Q9XYF5 ID Q9XYF5 PRELIMINARY; PRT; 265 AA.  
AC Q9XYF5;  
DT 01-NOV-1999 (TEMBLrel. 12, Created)  
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)  
DE BRACHYURY HOMOLOG HYBRAL (FRAGMENT).  
GN HYBRAL.  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;  
OC Hydridae; Hydra.  
OX NCBI\_TaxID=6087;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ZURICH;  
RX MEDLINE=99128189; PubMed=9927600;  
RA Technau U., Bode H.R.;  
RT "HybrAl, a Brachyury homologue, acts during head formation in Hydra.";  
RL Development 126:999-1010(1999).  
DR EMBL; AF105065; AAD26626.1; -;  
DR HSSP; P24781; IxBR.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.

DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
FT NON\_TER 265 265  
SQ SEQUENCE 265 AA; 30288 MW; C61B6B5EAAFP33545 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 265;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||

Db 118 VYIHP 122

RESULT 12

Q9HA44 ID Q9HA44 PRELIMINARY; PRT; 295 AA.  
AC Q9HA44;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
DE CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS TRANSCRIPTION FACTOR TBX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY GLAND;  
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK023330; BAB14014.1; -;  
DR HSSP; P24781; IxBR.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
SQ SEQUENCE 295 AA; 33197 MW; F2BD3E53E0ED21E0 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5  
|||||

Db 172 VYIHP 176

RESULT 13

O96040 ID O96040 PRELIMINARY; PRT; 295 AA.  
AC O96040;  
DT 01-MAY-1999 (TEMBLrel. 10, Created)  
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)  
DE PFBRAL.  
OS Ptychodera flava.  
OC Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychoderidae;  
OC Ptychodera.  
OX NCBI\_TaxID=63121;

```

RN SEQUENCE FROM N.A.
RX MEDLINE=98413048; PubMed=9739128;
RA Tagawa K., Humphreys T., Satoh N.;
RT "Novel pattern of Brachyury gene expression in hemichordate embryos.";
RL Mech. Dev. 75:139-143(1998).
DR EMBL; AB004912; BAA37091.1; -.
DR HSSP; P24781; 1XBR.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
SQ SEQUENCE 295 AA; 33331 MW; 3438B0D0B4F1EE75 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5
Db 96 VYIHP 100

RESULT 14
Q923Q5 PRELIMINARY; PRT; 317 AA.
AC Q923Q5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DMS38M10.7 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY)
DE (OLFACATORY RECEPTOR LIKE) PROTEIN).
GN DMS38M10.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RA Kay M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136158; CAC43450.1; -.
KW Receptor; Transmembrane.
SQ SEQUENCE 317 AA; 34674 MW; 763C856543F7327A CRC64;

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Query Match 100.0%; Score 30; DB 11; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5
Db 257 VYIHP 261

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RESULT 15
Q9VZ11 PRELIMINARY; PRT; 323 AA.
AC Q9VZ11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CG12624 PROTEIN.
GN CG12624.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Ananadides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pah S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003485; AAF48020.1; -.
DR FlyBase; FBgn030284; CG12624.
DR InterPro; IPR001320; Ion_glut_receptor.
DR Pfam; PF00060; lig_chan; 1.
SQ SEQUENCE 323 AA; 36569 MW; 29948CFA8E818A38 CRC64;

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Query Match 100.0%; Score 30; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYIHP 5
Db 168 VYIHP 172

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Search completed: July 1, 2002, 07:45:12
Job time: 408 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 seconds  
(without alignments)  
4.211 Million cell updates/sec

Title: US-09-723-197-8

Perfect score: 34

Sequence: 1 DRVYIH 6

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	6	17 AAR95669	Angiotensin II fra
2	34	100.0	6	19 AAW65604	Angiotensin II ana
3	34	100.0	6	19 AAW64735	Angiotensin II pep
4	34	100.0	6	19 AAW71117	Peptide AII(1-6) u
5	34	100.0	6	20 AAY49593	Angiotensin analog
6	34	100.0	6	20 AAY33908	Angiotensin II ana
7	34	100.0	6	20 AAY30546	Amino acid sequenc
8	34	100.0	6	20 AAY30590	Amino acid sequenc
9	34	100.0	6	20 AAY32721	Angiotensin II ana
10	34	100.0	6	20 AAY33775	Angiotensin II (AI
11	34	100.0	6	20 AAY15352	Angiotensin II (AI

12	34	100.0	6	20 AAY15312	Angiotensin II (AI
13	34	100.0	6	21 AAB27408	Angiotensin II ana
14	34	100.0	6	21 AAB28106	Angiotensin II ana
15	34	100.0	6	21 AAY84131	Peptide comprising
16	34	100.0	6	21 AAY77044	Angiotensin II (AI
17	34	100.0	6	21 AAY57408	Angiotensin peptid
18	34	100.0	6	22 AAE08878	AII peptide (resid
19	34	100.0	6	22 AAE02995	Human angiotensin
20	34	100.0	6	22 AAE03158	Human angiotensin
21	34	100.0	7	17 AAR95665	Angiotensin II fra
22	34	100.0	7	19 AAW56600	Angiotensin II ana
23	34	100.0	7	19 AAW64731	Angiotensin II pep
24	34	100.0	7	19 AAW71113	Peptide AII(1-7) u
25	34	100.0	7	20 AAY49589	Angiotensin analog
26	34	100.0	7	20 AAY50296	Neutrophil-activat
27	34	100.0	7	20 AAY33904	Angiotensin II ana
28	34	100.0	7	20 AAY30542	Amino acid sequenc
29	34	100.0	7	20 AAY30586	Amino acid sequenc
30	34	100.0	7	20 AAY32717	Angiotensin II ana
31	34	100.0	7	20 AAY33771	Angiotensin II (AI
32	34	100.0	7	20 AAY15348	Angiotensin II (AI
33	34	100.0	7	20 AAY15308	Angiotensin II (AI
34	34	100.0	7	21 AAB26205	Anion exchange res
35	34	100.0	7	21 AAB27404	Angiotensin II ana
36	34	100.0	7	21 AAB28102	Angiotensin II ana
37	34	100.0	7	21 AAY84565	Amino acid sequenc
38	34	100.0	7	21 AAY84127	Peptide comprising
39	34	100.0	7	21 AAY77040	Angiotensin II (AI
40	34	100.0	7	21 AAY57404	Angiotensin peptid
41	34	100.0	7	22 AAE08874	AII peptide (resid
42	34	100.0	7	22 AAE02991	Human angiotensin
43	34	100.0	7	22 AAE03154	Human angiotensin
44	34	100.0	7	22 AAB91452	Angiotensin peptid
45	34	100.0	7	22 AAB91463	Angiotensin peptid

#### ALIGNMENTS

#### RESULT 1

AAR95669  
ID AAR95669 standard; peptide; 6 AA.  
AC AAR95669;  
XX  
XX  
DT 09-JAN-1997 (first entry)  
DT Angiotensin II fragment AII(1-6).  
DE  
DE Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;  
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;  
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.  
XX  
XX Synthetic.  
OS  
XX  
XX WO9614858-A1.  
PN  
XX  
PD 23-MAY-1996.  
XX  
XX  
PF 14-NOV-1995; 95WO-US14764.  
PF  
PR 06-JUN-1995; 95US-0465775.  
PR 14-NOV-1994; 94US-0337781.  
XX  
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX  
XX Dizerega GS, Rodgers K;  
XX  
XX WPI; 1996-259561/26.  
XX  
XX Accelerating wound healing by application of angiotensin II  
XX fragments - are effective at very low concn. and do not cause  
XX hypertension

XX Disclosure; Page 4; 46pp; English.

XX

CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see

CC AAR95662) is an octapeptide present in humans and other species. AT2 is

CC one of the most potent vasoconstrictors known, causing constriction of

CC the arterioles. The formation of angiotensin is initiated by the action

CC of renin on angiotensinogen. The substance formed is a decapeptide

CC called angiotensin I which is converted by the enzyme angiotensinase (by

CC removal of the C-terminal His-leu) into AT2. AT2 increases the release

CC of extracellular matrices involved in wound repair. These fragments can

CC be used in a compound for accelerating wound healing. The compounds are

CC administered as matricial or micellar solutions, formulated with a

CC carrier or diluent, alternatively the compound is applied in conjuncture

CC with a wound dressing. The carrier used in the composition is

CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly

CC glycols. By using fragments of this sequence (or analogues of it),

CC growth as well as healing of tissues is improved, such as in cases of

CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or

CC intraperitoneal surgical wounds. The compounds containing the AT2

CC fragments are less hypertensive than full length AT2, and are also

CC effective at much lower (nanomolar) concentrations than full length AT2.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 17; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
| | | | |

Db 1 drvyih 6

## RESULT 2

AAW65604

ID AAW65604 standard; peptide; 6 AA.

XX

AC AAW65604;

XX

DT 09-NOV-1998 (first entry)

XX

DE Angiotensin II analogue, AII(1-6).

XX

KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;

KW wound healing.

XX Synthetic.

OS Homo sapiens.

XX WO9826795-A1.

XX 25-JUN-1998.

XX 16-DEC-1997; 97WO-US23461.

XX 15-DEC-1997; 97US-0990664.

XX 16-DEC-1996; 96US-0028310.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega GS, Rodgers KE;

XX WPI; 1998-362518/31.

XX Promoting incorporation of skin graft onto underlying tissue -

PT comprises pre-treating graft with angiotensin II, or analogue or

PT peptide fragment

XX Disclosure; Page 6; 82pp; English.

XX The invention relates to the use of angiotensin II (AII), AII analogues,

CC AII fragments and AII fragment analogues for promoting incorporation of a

CC skin graft into underlying tissue of a mammal. The peptides are effective

CC in accelerating the growth or healing of skin grafts and in accelerating

CC re-epithelialisation and tissue repair, even at very low concentrations.

CC They can significantly accelerate the rate of healing at nanomolar levels

CC in vivo. AII accelerates wound repair by increased neovascularisation,

CC growth factor release, re-epithelialisation, extracellular matrix production

CC and increased flow of blood and nutrients to the injured tissue. Use of

CC the above peptides other than AII itself (an extremely potent vaso-

CC constrictor) may avoid the side-effects of AII, such as increase in blood

CC pressure and thirst. The present sequence represents an angiotensin

CC II fragment.

SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 19; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
| | | | |

Db 1 drvyih 6

## RESULT 3

AAW64735

ID AAW64735 standard; peptide; 6 AA.

XX AAW64735;

XX 02-NOV-1998 (first entry)

XX Angiotensin II peptide #7.

XX Proliferation; mesenchymal stem cell; lineage-specific cell;

KW haematopoietic; cell culture; transplantation; treatment; malignant;

KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.

XX Synthetic.

OS Homo sapiens.

XX WO9832457-A2.

XX 30-JUL-1998.

XX 26-JAN-1998; 98WO-US01552.

XX 23-JAN-1998; 98US-0066593.

XX 28-JAN-1997; 97US-0036507.

XX 08-MAY-1997; 97US-0046859.

XX 28-OCT-1997; 97US-0063684.

XX 31-OCT-1997; 97US-0063910.

XX 18-NOV-1997; 97US-0065612.

XX 26-NOV-1997; 97US-0066593.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1998-437044/37.

XX Promoting haematopoietic and mesenchymal cell proliferation and

PT differentiation - by contacting the cells with angiotensinogen,

PT angiotensin I or II, or analogues or fragments of these

XX Claim 7; Page 14; 114pp; English.

XX AAW64728-W64763 are peptides used in a novel method for accelerating the

CC proliferation of mesenchymal stem cells (MSCs), haematopoietic

CC lineage-specific cells or mesenchymal lineage-specific cells. The method

CC involves contacting the cells with an active agent comprising a sequence

CC consisting of at least three contiguous amino acids of groups R1-R8 in



the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val, Ala, Leu, norleu, ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoSer or azoTyr, R5 = Ile, Ala, Leu, norleu, Val or Gly; R6 = His, Arg or 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are not defined in the specification, the peptide bond between Ra and Rb is labile to aminopeptidase A cleavage excluding sequences including R4 as a terminal Tyr group. A second active agent comprising a sequence consisting of at least three contiguous amino acids of groups R2-R8 in the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala, Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also described. The inventions are particularly useful in cell culture mediums. These cells may be used in transplantation techniques for treatment of malignant or inherited diseases. The formulae represent analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII), or AII AT2 type 2 receptor agonists.

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRVYIH 6  
| | | | |

Db 1 drvyih 6

RESULT 4

AAW71117  
ID AAW71117 standard; peptide; 6 AA.

AC AAW71117;

DT 27-OCT-1998 (first entry)

DE Peptide AII(1-6) used to accelerate thermal wound healing.

KW Angiotensin; AII; acceleration; thermal wound healing; human;

KW growth factor release; neovascularisation; re-epithelialisation;

KW extracellular matrix production.

OS Synthetic.

PN WO9833813-A2.

PD 06-AUG-1998.

PF 04-FEB-1998; 98WO-US02049.

PR 04-FEB-1997; 97US-0037166.

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

PI DiZerega G, Rodgers KE;

DR WPT; 1998-437391/37.

PT Methods for accelerating thermal wound healing in humans - using angiotensinogen II and AII analogues

PS Claim 3; Page 9; 58pp; English.

CC AAW71110-27 represent peptide used in the method of the invention. The specification describes a method of accelerating thermal wound healing in humans. The method comprises applying to the thermally injured tissue an amount of at least one active agent which comprises the peptides AAW71115-27. The method can be used to promote the healing of thermal wounds by accelerating growth factor release, neovascularisation, re-epithelialisation and extracellular matrix production. The sequences are analogues of the angiotensin or angiotensinogen family of proteins.

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRVYIH 6  
| | | | |

Db 1 drvyih 6

RESULT 5

AAAY49593  
ID AAY49593 standard; peptide; 6 AA.

AC AAY49593;

DT 13-JAN-2000 (first entry)

DE Angiotensin analogue peptide SEQ ID NO:8.

KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection; receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.

OS Synthetic.

PN WO9952540-A1.

PD 21-OCT-1999.

PF 07-APR-1999; 99WO-US07654.

PR 09-APR-1998; 98US-0081262.

PR 12-JUN-1998; 98US-0089024.

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

PI Rodgers KE, Dizerega G;

DR WPT; 1999-620285/53.

PT Treating or preventing infections in mammals using peptides derived from angiotensin or angiotensin receptor agonists

PS Claim 2; Page 10; 91pp; English.

CC The present invention describes a method for treating or preventing infections in mammals by administering peptides (A) that are fragments or analogues (or their fragments) of angiotensinogen, angiotensins I or II, or angiotensin II AT<sub>2</sub>-type receptor agonists. (A) contain at least 3 consecutive amino acids (aa) from the sequence (S1):

R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-; X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asp, Acpc (1-aminocyclopentane carboxylic acid), Ala, dimethylglycine, pro, betaine, Glu(NH<sub>2</sub>), Gly, Asp(NH<sub>2</sub>) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser, sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys, Ile, Gly, Pro, Alb (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr (Optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr; R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe; R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso = sequences having R4 as a terminal Tyr residue are excluded. The method is particularly used in cases of bacterial infection (e.g. septic shock, peritonitis, bacteraemia or endotoxaemia) but also against viral and parasitic infections. AAY49586 to AAY49623 represent specifically claimed examples of (A).

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||

Db 1 drvyih 6

# RESULT 6

AA33908

ID AAY33908 standard; peptide; 6 AA.

XX

AC AAY33908;

XX

DT 29-NOV-1999 (first entry)

XX

DE Angiotensin II analogue AII(1-6).

XX

KW embryonic stem cell; ES; angiotensin; totipotent cell;

KW gene therapy; replacement therapy; angiotensin II; AII;

KW analogue.

XX

OS Homo sapiens.

XX

PN WO942122-A1.

XX

PD 26-AUG-1999.

XX

PF 16-FEB-1999; 99WO-US03243.

XX

PR 19-FEB-1998; 98US-0075179.

XX

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX

PI Dizerega G, Rodgers KE;

XX

XX WPI; 1999-527419/44.

DR

PT Promoting embryonal cell proliferation, using angiotensinogen and

XX angiotensin peptides, analogs or fragments

XX

PS Claim 2; Page 8; 76pp; English.

XX

CC This is the amino acid sequence of the Angiotensin II analogue, AII(5-8). The formation of Angiotensin II (AII) is initiated by the action of renin on the plasma substrate angiotensinogen.

CC This results in Angiotensin I (AI) which then converted to AII by the

CC converting enzyme angiotensinase which removes the C-terminal His-Leu

CC residues from AI (AAY42372).

CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and

CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,

CC or AII AT2 type 2 receptor agonists can rapidly provide a large

CC population of ESCs (Embryonic Stem Cell) for use in replacement therapy.

CC Similarly, methods that increase in vivo proliferation of ESCs will

CC enhance the utility of replacement therapy by rapidly increasing local

CC concentration of the stem cells and their progeny at the site of

CC therapy. The method also increases the potential utility of ESCs as

CC vehicles for gene therapy in certain disorders by more efficiently

CC providing a large number of such cells for transfection, and also by

CC providing a more efficient means to rapidly expand transacted ESCs.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6

|||||

Db 1 drvyih 6

# RESULT 7

AA30590

ID AAY30590 standard; peptide; 6 AA.

XX

AC AAY30590;

XX

DT 18-NOV-1999 (first entry)

XX

DE Amino acid sequence of an angiotensin II (AII) fragment AII1-6.

XX

KW Angiotensin; analogue; radiation mitigation; tissue damage;

KW radiation therapy; bone marrow transplantation;

KW megakaryocyte production; platelet production; cancer therapy;

KW gene therapy; hematopoietic disorder.

AA30546

ID AAY30546 standard; peptide; 6 AA.

XX

AC AAY30546;

XX

DT 18-NOV-1999 (first entry)

XX

DE Amino acid sequence of angiotensin II fragment AII1-6.

XX

KW Angiotensin; analogue; tissue equivalent; cell proliferation.

XX

OS Synthetic.

XX

PN WO9946285-A2.

XX

PD 16-SEP-1999.

XX

PF 11-MAR-1999; 99WO-US05261.

XX

PR 11-MAR-1998; 98US-0077499.

XX

PR 12-JUN-1998; 98US-0089064.

XX

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX

PI Rodgers KE, Dizerega G;

XX

DR WPI; 1999-551360/46.

XX

PT An improved method for producing a tissue equivalent with angiotensin I

XX and II derived active agents -

PS Claim 2; Page 55; 83pp; English.

XX

CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII fragments and AII analogues. The peptides are used in the method of the invention. The specification describes an improved method for producing a tissue equivalent. The method comprises contacting the tissue equivalent with angiotensin I and II derived active agents. The methods are used for production and culture of tissue equivalents (three-dimensional cell and tissue culture systems),

CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,

CC vascular graft, cartilage, ligament, collagen lattice, liver and

CC kidney tissue equivalents. The methods and tissue culture systems

CC are used for the long-term proliferation of cells and tissues

CC in an in vitro environment that more closely approximates that found

XX in vivo.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6

|||||

Db 1 drvyih 6

# RESULT 8

AA30590

ID AAY30590 standard; peptide; 6 AA.

XX

AC AAY30590;

XX

DT 18-NOV-1999 (first entry)

XX

DE Amino acid sequence of an angiotensin II (AII) fragment AII1-6.

XX

KW Angiotensin; analogue; radiation mitigation; tissue damage;

KW radiation therapy; bone marrow transplantation;

KW megakaryocyte production; platelet production; cancer therapy;

KW gene therapy; hematopoietic disorder.

XX OS Synthetic.  
 XX PN W09945945-A1.  
 XX PD 16-SEP-1999.  
 XX PF 08-MAR-1999; 99WO-US05194.  
 XX PR 10-MAR-1998; 98US-0077382.  
 XX PR 09-APR-1998; 98US-0081262.  
 XX PR 30-APR-1998; 98US-0083670.  
 XX PR 19-JUN-1998; 98US-0090096.  
 XX PR 22-JUN-1998; 98US-0090216.  
 XX PR 11-SEP-1998; 98US-0099957.  
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PA (RODG/) RODGERS K E.  
 XX PA (DIZE/) DIZEREGA G.  
 XX PI Rodgers KE, Dizerega G;  
 XX PS WPI; 1999-551209/46.  
 XX PT Use of angiotensin and angiotensin type peptides, for mitigating  
 PT radiation induced tissue damage, improving bone marrow transplantation  
 PT and promoting megakaryocyte and platelet production  
 XX PS Claim 2; Page 88; 116pp; English.  
 XX CC AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII  
 CC fragments and AII analogues. The peptides are used in the method  
 CC of the invention. The specification describes a method for mitigating  
 CC radiation induced tissue damage, improving the effectiveness of  
 CC radiation therapy, to support bone marrow transplantation, and  
 CC promoting megakaryocyte production and mobilization and platelet  
 CC production. The method comprises administration of the present peptides.  
 CC The methods can be used to mitigate radiation induced tissue damage, to  
 CC improve the effectiveness of radiation therapy, to support bone marrow  
 CC transplantation, and to promote megakaryocyte production and  
 CC mobilization and platelet production. They are used particularly in  
 CC cancer therapy. They can also be used to provide megakaryocytes as  
 CC vehicles for gene therapy in hematopoietic disorders, by providing a  
 CC more efficient means to rapidly expand transfected megakaryocytes.  
 XX SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
 |||||  
 Db 1 drvyih 6

RESULT 9  
 AAY32721  
 ID AAY32721 standard; peptide; 6 AA.  
 XX AC AAY32721;  
 XX DT 09-NOV-1999 (first entry)  
 XX DE Angiotensin II analogue AII(1-6).  
 XX KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;  
 KW chemotaxis; growth factor; liver regeneration; cirrhosis;  
 KW hepatocarcinoma; hepatectomy; transplantation.  
 XX OS Synthetic.  
 OS Homo sapiens.

XX WO9939743-A2.  
 XX PN 12-AUG-1999.  
 XX PD 08-FEB-1999; 99WO-US02618.  
 XX PF 13-NOV-1998; 98US-0108412.  
 XX PR 09-FEB-1998; 98US-0074104.  
 XX PA (DIZE/) DIZEREGA G.  
 XX PA (RODG/) RODGERS K E.  
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PI Dizerega G, Rodgers KE;  
 XX PS WPI; 1999-508461/42.  
 XX PT Hepatic cell proliferation with angiotensin I and II derived active  
 PT agents, useful for regeneration of liver after resection  
 XX PS Claim 2; Page 9; 66pp; English.  
 XX CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The  
 CC peptides are derived from the AII peptide (AAY32750). AII increases  
 CC mitogenesis and chemotaxis in cultured cells, and also increases the  
 CC release of growth factors and extracellular matrices. AII has also been  
 CC shown to increase the proliferation of certain cell types. The AII  
 CC analogue peptides can be used as the active agent in a method for  
 CC promoting hepatic cell proliferation and differentiation. The method  
 CC involves contacting the hepatic cells with an amount effective enough to  
 CC promote proliferation of any of the peptides. This method is useful in  
 CC liver regeneration following resection of hepatocarcinomas, hepatitis  
 CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic  
 CC failure, hepatocyte transplantation, liver transplantation and other  
 CC hepatic disorders where rapid regeneration of the liver is desirable. The  
 CC methods are also useful in rapidly providing a large population of  
 CC hepatic cells for use in cell therapy and for providing a large  
 CC population of transfected hepatic cells for use in gene therapy.  
 XX SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
 |||||  
 Db 1 drvyih 6

RESULT 10  
 AAY33775  
 ID AAY33775 standard; peptide; 6 AA.  
 XX AC AAY33775;  
 XX DT 09-NOV-1999 (first entry)  
 XX DE Angiotensin II (AII) octapeptide fragment AII(1-6).  
 XX KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;  
 KW neuronal cell proliferation; differentiation; Alzheimer's disease;  
 KW Parkinson's disease; neuron replacement therapy.  
 XX OS Homo sapiens.  
 XX PN W09942123-A1.  
 XX PD 26-AUG-1999.  
 XX PF 19-FEB-1999; 99WO-US03772.

XX 19-FEB-1998; 98US-0075232.  
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX Dizerega G, Rodgers KE;  
XX WPI; 1999-527420/44.  
XX Promoting neuronal cell proliferation and differentiation  
XX Claim 2; Page 10; 62pp; English.  
XX Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The application of angiotensin to wound tissue significantly increases the rate of wound healing. AII is known to increase mitogenesis and chemotaxis in cultured cells, and also increases their release of growth factors and extracellular matrices, implicating it in cell growth and differentiation. AT2 receptors are receptors for AII and are thought to be involved in the mediation of the cell differentiation effects of AII. Peptides AAY33768-Y33802 are used in a method for promoting neuronal cell proliferation or differentiation. This method is useful in the treatment of Alzheimer's and Parkinson's diseases by neuron replacement therapy.  
XX Sequence 6 AA;  
SQ

Query Match 100.0%; Score 34; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
DB 1 drvylh 6

RESULT 11  
AAY15352  
ID AAY15352 standard; peptide; 6 AA.  
XX  
AC AAY15352;  
XX  
DT 09-NOV-1999 (first entry)  
XX  
DE Angiotensin II (AII) analogue, AII(1-6).  
XX  
KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;  
KW AII; analogue; chronic renal failure; cancer; bone marrow.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9940106-A2.  
XX  
PD 12-AUG-1999.  
XX  
PF 08-FEB-1999; 99WO-US02648.  
XX  
PR 09-DEC-1998; 98US-0111535.  
PR 09-FEB-1998; 98US-0074106.  
XX  
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX Dizerega G, Rodgers KE;  
XX WPI; 1999-508486/42.  
XX Promoting erythropoiesis with angiotensin I and II derived active agents, useful for treatment of, e.g. congenital or acquired aplastic or hypoplastic anemia

PS Claim 2; Page 10; 76pp; English.  
XX This sequence is an angiotensin II (AII) analogue. Similar sequences also based on the AII peptide have been tested against each other, AII and a negative control. These active agents have been shown to affect the levels of BFU-E (burst forming units-erythroid) in culture. The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380) augment erythropoiesis by potentiating erythropoietin-induced differentiation. Increasing the rate of erythropoiesis improves clinical benefits for the treatment of congenital or acquired aplastic or hypoplastic anemia associated with chronic renal failure, end-stage renal disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy, bone marrow transplantation and chronic diseases.  
XX The active agents permit the use of smaller doses of erythropoietin therefore decreasing treatment costs.  
XX Sequence 6 AA;  
SQ

Query Match 100.0%; Score 34; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
DB 1 drvylh 6

RESULT 12  
AAY15312  
ID AAY15312 standard; peptide; 6 AA.  
XX  
AC AAY15312;  
XX  
DT 09-NOV-1999 (first entry)  
XX  
DE Angiotensin II (AII) analogue, AII(1-6).  
XX  
KW angiotensin; angiotensin II; AII; wound healing; scarring;  
KW tissue repair; agonist; analogue.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9940107-A2.  
XX  
PD 12-AUG-1999.  
XX  
PF 08-FEB-1999; 99WO-US02725.  
XX  
PR 09-FEB-1998; 98US-0074105.  
XX  
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX Dizerega G, Rodgers KE;  
XX WPI; 1999-508487/42.  
XX Epithelial stem cell and keratinocyte proliferation with angiotensin I and II derived active agents, useful for treatment of skin wounds  
XX Claim 2; Page 10; 70pp; English.  
XX This is the amino acid sequence of an Angiotensin II analogue. This and other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337) can be used to promote the proliferation of epithelial stem cells and keratinocytes leading to a more rapid and efficient cellular response to stratified epithelial injury. The angiotensin analogues are derived from an octapeptide present in humans and other species which has the sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as angiotensin II (AII). This is formed by the action of renin on the plasma substrate angiotensinogen, the product of this reaction is a decapeptide called angiotensin I (AI) which is converted to AII by the

CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
CC residues from AI (AAY15339).

XX  
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
| | | | |  
Db 1 drvyih 6

RESULT 13  
AAB27408  
ID AAB27408 standard; Peptide; 6 AA.

XX AC AAB27408;

XX DT 23-JAN-2001 (first entry)

XX DE Angiotensin II analog AII(1-6).

XX KW Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;  
XX KW cardiomyopathies; inflammation; infection; sepsis; ischemia;  
XX KW heart valve disease; myocarditis; angiotensin.

XX OS Synthetic.

XX PN W0200053211-A2.

XX PD 14-SEP-2000.

XX PF 09-MAR-2000; 2000WO-US06198.

XX PR 09-MAR-1999; 99US-0123678.

XX PR 31-AUG-1999; 99US-0151874.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers K, Dizerega G;

XX DR WPI; 2000-611400/58.

XX PT Promoting myocyte proliferation and myocardial tissue repair by  
XX PT contacting myocytes with angiotensinogen or angiotensin I or II, useful  
XX PT for treating heart attacks, cardiomyopathies, inflammation and  
XX PT infection.

XX PS Claim 2; Page 10; 55pp; English.

XX CC The present invention relates to a method of promoting myocyte  
XX CC proliferation or differentiation by contacting myocytes with an active  
XX CC agent containing angiotensinogen, angiotensin I and II (AI, AII), and  
XX CC angiotensin analogs. The present sequence is an angiotensin II analog  
XX CC of the invention. The active agents of the invention may be useful for  
XX CC promoting myocardial tissue repair following myocardial injury and for  
XX CC treating heart failure in a mammal. Administration to accelerate in  
XX CC vivo myocyte proliferation and/or to treat myocardial injuries can be  
XX CC used to treat cardiomyopathies, inflammation, infection, sepsis,  
XX CC ischemia, heart valve disease, myocarditis, inflammation, myocardial  
XX CC ischemia and infarction and for improving cardiac output by increasing  
XX CC stroke volume.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
| | | | |  
Db 1 drvyih 6

RESULT 14  
AAB28106  
ID AAB28106 standard; Peptide; 6 AA.  
XX AC AAB28106;  
XX DT 26-JAN-2001 (first entry)  
XX DE Angiotensin II analogue SEQ ID NO: 8.

XX KW Wound; scar formation; healing; adhesion formation; AII;  
XX KW angiotensin II analogue; scar treatment.  
XX OS Synthetic.

XX PN W0200056345-A2.

XX PD 28-SEP-2000.

XX PF 22-MAR-2000; 2000WO-US07669.

XX PR 23-MAR-1999; 99US-0125707.

XX PR 16-JUN-1999; 99US-0139541.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers K, Dizerega G;

XX DR WPI; 2000-587607/55.

XX PT Limiting scar or adhesion formation comprises administering at least  
XX PT one active agent comprising a peptide.

XX PS Claim 2; Page 10; 54pp; English.

XX CC The present invention is concerned with peptide analogues of angiotensin  
XX CC II (AII) which can be used to limit scar and adhesion formation. The  
XX CC application of AII to wound tissue results in a rapid increase in the  
XX CC rate of wound healing and causes the proliferation of certain cells, such  
XX CC as epithelial cells and keratinocytes. Analogues of the protein have been  
XX CC shown to reduce scar formation, and can be used not only to limit new  
XX CC scar formation but also to therapeutically treat existing scars. The  
XX CC wound types include lacerations, burns, punctures, trauma, ulcers,  
XX CC periodontal conditions, laparotomy and incisional wounds, revision of  
XX CC hypertrophic scars, genetic hypertrophic scars, keloid scars,  
XX CC contractures after burns and cosmetic surgical procedures.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
| | | | |  
Db 1 drvyih 6

RESULT 15  
AAY84131  
ID AAY84131 standard; peptide; 6 AA.

XX AC AAY84131;

XX DT 03-JUL-2000 (first entry)

XX DE Peptide comprising amino acids 1-6 of angiotensin II.

XX Angiotensin III; angiotensinogen; angiotensin I; angiotensin II;  
 KW analogue; blood flow; ischemic tissue; angiogenesis; cardiac remodelling;  
 KW congestive heart disease; ischemic myocardial infarction;  
 KW embryonic development; wound healing; chronic inflammatory disease.  
 OS Synthetic.  
 XX WO200009144-A1.  
 XX 24-FEB-2000.  
 XX 12-AUG-1999; 99WO-US18374.  
 XX 13-AUG-1998; 98US-0096414.  
 PR 18-SEP-1998; 98US-0101024.  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PA Rodgers K, Dizerega G;  
 PI WPI; 2000-237409/20.  
 XX Increasing blood flow to ischemic tissue for minimizing cardiac  
 PT remodelling and development of congestive heart failure involves  
 PT administration of an active agent  
 XX Claim 2; Page 42; 56pp; English.  
 CC The present sequence represents an angiotensin II fragment. The  
 CC specification also describes peptides derived from angiotensinogen,  
 CC angiotensin I, angiotensin II, angiotensin III, and their analogues.  
 CC The peptides are used for increasing blood flow to ischemic tissue.  
 CC The peptides are angiogenesis stimulators. The peptides are useful for  
 CC increasing blood flow to ischemic tissue by stimulating angiogenesis,  
 CC and minimizing cardiac remodelling and development of congestive heart  
 CC disease following a ischemic myocardial infarction. The stimulation of  
 CC angiogenesis is also useful for embryonic development, wound healing  
 CC and treating chronic inflammatory disease.  
 XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYIH 6  
 Db 1 drvylh 6

Search completed: July 1, 2002, 07:41:55  
 Job time: 347 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:00 ; Search time 59.1 Seconds  
(without alignments)  
2.480 Million cell updates/sec

Title: US-09-723-197-8  
Perfect score: 34  
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	6	2	US-08-465-775-8
2	34	100.0	6	3	US-09-208-337-8
3	34	100.0	6	3	US-08-990-664-9
4	34	100.0	6	4	US-09-373-962-8
5	34	100.0	6	4	US-09-245-680-8
6	34	100.0	6	4	US-09-198-806C-8
7	34	100.0	6	4	US-09-352-191-8
8	34	100.0	6	4	US-09-012-400-8
9	34	100.0	7	2	US-08-465-775-4
10	34	100.0	7	3	US-08-990-664-5
11	34	100.0	7	4	US-09-373-962-4
12	34	100.0	7	4	US-09-245-680-4
13	34	100.0	7	4	US-09-198-806C-4
14	34	100.0	7	4	US-09-352-191-4
15	34	100.0	7	4	US-09-012-400-4
16	34	100.0	7	6	5451571-4
17	34	100.0	8	1	US-07-858-842-2
18	34	100.0	8	1	US-08-021-839A-3
19	34	100.0	8	1	US-08-184-935-2
20	34	100.0	8	1	US-08-212-433A-29
21	34	100.0	8	1	US-08-185-448-8
22	34	100.0	8	1	US-07-776-272-1
23	34	100.0	8	1	US-08-428-488-21
24	34	100.0	8	1	US-08-337-781-1
25	34	100.0	8	1	US-08-240-711-20
26	34	100.0	8	1	US-08-594-117-1
27	34	100.0	8	1	US-08-594-117-1

28	34	100.0	8	1	US-08-520-770-2	Sequence 2, Appli
29	34	100.0	8	1	US-08-457-753-20	Sequence 20, Appli
30	34	100.0	8	2	US-08-115-968-1	Sequence 1, Appli
31	34	100.0	8	2	US-08-115-968-3	Sequence 3, Appli
32	34	100.0	8	2	US-08-115-968-4	Sequence 4, Appli
33	34	100.0	8	2	US-08-465-774-1	Sequence 1, Appli
34	34	100.0	8	2	US-08-360-784B-2	Sequence 2, Appli
35	34	100.0	8	2	US-08-623-833B-4	Sequence 4, Appli
36	34	100.0	8	2	US-08-465-775-1	Sequence 1, Appli
37	34	100.0	8	2	US-08-542-927-3	Sequence 3, Appli
38	34	100.0	8	3	US-08-716-256-29	Sequence 29, Appli
39	34	100.0	8	3	US-09-054-308A-2	Sequence 2, Appli
40	34	100.0	8	3	US-09-280-047-7	Sequence 7, Appli
41	34	100.0	8	3	US-09-208-337-1	Sequence 1, Appli
42	34	100.0	8	3	US-08-990-664-1	Sequence 1, Appli
43	34	100.0	8	3	US-08-990-664-29	Sequence 29, Appli
44	34	100.0	8	3	US-08-990-664-30	Sequence 30, Appli
45	34	100.0	8	3	US-08-927-128-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1  
US-08-465-775-8  
; Sequence 8, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-775-8

Query Match 100.0%; Score 34; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYIH 6  
DB 1 DRVYIH 6

RESULT 2  
US-09-208-337-8  
; Sequence 8, Application US/09208337  
; Patent No. 6096709  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: Gere, dizerega  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,337  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,775  
; FILING DATE: 06-JUN-1995  
; APPLICATION NUMBER: 08/337,781  
; FILING DATE: 14-NOV-1994  
; APPLICATION NUMBER: 08/126,368  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC010.001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 949-760-0404  
; TELEFAX: 949-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-09-208-337-8

Query Match 100.0%; Score 34; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
| | | | |  
DB 1 DRVYIH 6

RESULT 3  
US-08-990-664-9  
; Sequence 9, Application US/08990664  
; Patent No. 6110895  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
; TITLE OF INVENTION: IN SKIN GRAFTS  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/990,664  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/028,310  
; FILING DATE: 16-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC012.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-760-0404  
; TELEFAX: 714-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-990-664-9

Query Match 100.0%; Score 34; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
| | | | |  
DB 1 DRVYIH 6

RESULT 4  
US-09-373-962-8  
; Sequence 8, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-373-962-8

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
| | | | |  
DB 1 DRVYIH 6



RESULT 5  
US-09-245-680-8  
; Sequence 8, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245,680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-245-680-8

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
| | | | |  
Db 1 DRVYIH 6

RESULT 6  
US-09-198-806C-8  
; Sequence 8, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-198-806C-8

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
| | | | |  
Db 1 DRVYIH 6

RESULT 7  
US-09-352-191-8  
; Sequence 8, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue

; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352,191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-352-191-8

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
| | | | |  
Db 1 DRVYIH 6

RESULT 8  
US-09-012-400-8  
; Sequence 8, Application US/09012400D  
; Patent No. 6335195  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell  
; TITLE OF INVENTION: Proliferation and Differentiation  
; FILE REFERENCE: 97,017-G  
; CURRENT APPLICATION NUMBER: US/09/012,400D  
; CURRENT FILING DATE: 1998-01-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-012-400-8

Query Match 100.0%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
| | | | |  
Db 1 DRVYIH 6

RESULT 9  
US-08-465-775-4  
; Sequence 4, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 595430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,775  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-360  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-775-4

Query Match 100.0%; Score 34; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
DB 1 DRVYIH 6

## RESULT 10

US-09-208-337-4  
Sequence 4, Application US/09208337  
Patent No. 6096709  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: Gere, dizegga  
TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/208,337  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,775  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: 08/337,781  
FILING DATE: 14-NOV-1994  
APPLICATION NUMBER: 08/126,368  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: US010.001CP2  
TELEPHONE: 949-760-0404

TELEFAX: 949-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-208-337-4

Query Match 100.0%; Score 34; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
DB 1 DRVYIH 6

## RESULT 11

US-08-990-664-5  
Sequence 5, Application US/08990664  
Patent No. 6110895  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: dizegga, Gere  
TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
TITLE OF INVENTION: IN SKIN GRAFTS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/990,664  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,310  
FILING DATE: 16-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: US012.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-990-664-5

Query Match 100.0%; Score 34; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6

Db 1 DRVYIH 6  
|||||

RESULT 12

US-09-373-962-4  
; Sequence 4, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-373-962-4

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
|||||

Db 1 DRVYIH 6

RESULT 13

US-09-245-680-4  
; Sequence 4, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245,680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-245-680-4

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
|||||

Db 1 DRVYIH 6

RESULT 14

US-09-198-806C-4  
; Sequence 4, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-198-806C-4

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
|||||

Db 1 DRVYIH 6

RESULT 15

US-09-352-191-4  
; Sequence 4, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352,191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-352-191-4

Query Match 100.0%; Score 34; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
|||||

Db 1 DRVYIH 6

Search completed: July 1, 2002, 07:43:01  
Job time: 302 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:29 ; Search time 69.93 seconds  
(without alignments)  
8.244 Million cell updates/sec

Title: US-09-723-197-8  
Perfect score: 34  
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR71:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	10	2 S65432	angiotensin I - ho
2	34	100.0	14	2 A01250	angiotensin precu
3	34	100.0	15	2 A60834	angiotensin I prec
4	34	100.0	476	1 JC2318	angiotensin precu
5	34	100.0	477	1 ANRT	angiotensin precu
6	34	100.0	477	1 A29978	angiotensin precu
7	34	100.0	485	1 ANHU	angiotensin precu
8	34	100.0	540	2 S72233	transcription fact
9	33	97.1	10	2 A60624	angiotensin I - Ja
10	33	97.1	10	2 A90917	angiotensin precu
11	33	97.1	10	2 A90345	angiotensin precu
12	33	97.1	178	2 B42845	3-hydroxybutyrate
13	32	94.1	11	2 S07207	Crinia-angiotensin
14	32	94.1	263	2 F84339	hypothetical prote
15	32	94.1	460	2 H69095	carbon monoxide de
16	31	91.2	363	2 A81016	transcription regu
17	30	88.2	116	2 T03472	conserved hypothet
18	30	88.2	344	2 A42345	3-hydroxybutyrate
19	30	88.2	457	2 JC5422	FK506-binding prot
20	30	88.2	471	2 B64099	undecaprenyl-phosp
21	30	88.2	500	2 T19743	hypothetical prote
22	30	88.2	510	2 E84094	2,3-bisphosphoglyc
23	30	88.2	625	1 TBBO	thrombin (EC 3.4.2
24	30	88.2	970	2 S01352	type III site-spec
25	30	88.2	1014	2 T18759	hypothetical prote
26	30	88.2	1069	1 KUHU	ferroxidase (EC 1.
27	29	85.3	111	2 E83566	hypothetical prote
28	29	85.3	157	2 G00016	FGF-receptor - com
29	29	85.3	211	2 T42603	gene 60 protein -

30 29 85.3 212 1 WZBEF2 gene 60 protein -  
31 29 85.3 216 2 T36491 probable gntR-fami  
32 29 85.3 250 2 C81341 pseudouridylylate sy  
33 29 85.3 274 2 F81350 formyltetrahydrofo  
34 29 85.3 277 2 E86229 hypothetical prote  
35 29 85.3 281 2 H81315 probable ribosomal  
36 29 85.3 289 2 C96610 hypothetical prote  
37 29 85.3 293 2 E71819 formyltetrahydrofo  
38 29 85.3 293 2 B64699 formyltetrahydrofo  
39 29 85.3 312 2 C82208 siroheme synthase  
40 29 85.3 337 2 T49431 endocephine related  
41 29 85.3 411 2 S14538 transition protein  
42 29 85.3 415 2 I65223 heparin-binding fi  
43 29 85.3 435 2 D71857 hypothetical prote  
44 29 85.3 435 2 B64658 hypothetical prote  
45 29 85.3 444 2 C89768 conserved hypothet

ALIGNMENTS

RESULT 1  
S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432  
R:Wiljffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen  
Eur. J. Biochem. 237, 414-423, 1996  
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte  
A:Reference number: S65431; MUID:96215437  
A:Accession: S65432  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <WLD>  
A>Note: the source is designated as Haematobia irritans exigua

Query Match 100.0% Score 34; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
|||||  
Db 1 DRVYIH 6

RESULT 2  
A01250  
angiotensin precursor - horse (fragment)  
C:Species: Equus caballus (domestic horse)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998  
C:Accession: A92775; A01250  
R:Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957  
A:Reference number: A92775  
A:Accession: A92775  
A:Molecule type: protein  
A:Residues: 1-14 <SKE>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0% Score 34; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
|||||  
Db 1 DRVYIH 6

```
RESULT 3
A:0834
N:Alternatn I precursor - dog (fragment)
N:Contains: angiotensin I
C:Species: angiotensin I
C:Date: 13-Jun-1993 #sequence_revision 13-Jun-1993 #text_change 13-Jun-1993
C:Accession: A93945; A90456; A01251
R:Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A:Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
C:Reference number: A93945; MUID:83169849
A:Accession: A93945
A:Molecule type: mRNA
A:Residues: 1-477 <OH>
A:Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A:Title: Rat angiotensinogen and Des(angiotensin)angiotensinogen: purification, char
A:Reference number: A90456; MUID:82091819
A:Accession: A90456
A:Molecule type: protein
A:Residues: 25-41 <BOU>
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C:Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-11 angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MPT>
F:25-34/Product: angiotensin I #status experimental <PP1>
F:25-32/Product: angiotensin II #status experimental <PP2>
F:26-32/Product: angiotensin III #status experimental <PP3>
F:295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6
DB 1 DRVYIH 6

RESULT 4
JC2318
N:Alternatn precursor - sheep
N:Alternatn names: angiotensinogen
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JC2318; A25406
R:Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
A:Title: Sequencing and expression of sheep angiotensinogen cDNA.
A:Reference number: JC2318; MUID:95072318
A:Accession: JC2318
A:Molecule type: mRNA
A:Residues: 1-476 <NAG>
A:Cross-references: DDBJ:DL17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183
A:Experimental source: liver
A:Note: the authors translated the codon TTC for residue 465 as Leu
R:Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
Eur. J. Biochem. 154, 597-601, 1986
A:Title: Purification and characterization of ovine angiotensinogen.
A:Reference number: A25406; MUID:86136099
A:Accession: A25406
A:Molecule type: protein
A:Residues: 25-37, 'X', 39 <FER>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:24-476/Product: angiotensinogen #status predicted <MPT>
F:25-34/Product: angiotensin #status predicted <MAT>
F:295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6
DB 25 DRVYIH 30

RESULT 5
ANRT
angiotensin precursor - rat
N:Contains: angiotensin I; angiotensin II; angiotensin III
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jun-1993 #sequence_revision 13-Jun-1993 #text_change 18-Jun-1999
C:Accession: A93945; A90456; A01251
R:Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A:Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
C:Reference number: A93945; MUID:83169849
A:Accession: A93945
A:Molecule type: mRNA
A:Residues: 1-477 <OH>
A:Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A:Title: Rat angiotensinogen and Des(angiotensin)angiotensinogen: purification, char
A:Reference number: A90456; MUID:82091819
A:Accession: A90456
A:Molecule type: protein
A:Residues: 25-41 <BOU>
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C:Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-11 angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MPT>

Query Match 100.0%; Score 34; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6
```

Db 25 DRVYIH 30  
|||||

## RESULT 7

ANHU

angiotensin precursor [validated] - human  
N:Alternate names: angiotensinogen  
N:Contains: angiotensin I; angiotensin II; angiotensin III  
C:Species: Homo sapiens (man)  
C:Date: 06-Jul-1982 #sequence-revision 19-Jan-1996 #text-change 08-Dec-2000  
C:Accession: A35203; A31362; I37168; A60825; I39462; A90487; A90226; I54281; A01  
R:Kukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami,  
J. Biol. Chem. 265, 7576-7582, 1990  
A:Title: Structure and expression of the human angiotensinogen gene. Identification of a  
A:Reference number: A35203; MUID:90237063  
A:Accession: A35203  
A:Molecule type: DNA  
A:Residues: 1-485 <FOK>  
A:Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327  
R:Gaillard, I.; Clausner, E.; Corvol, P.  
DNA 8, 87-99, 1989  
A:Title: Structure of human angiotensinogen gene.  
A:Reference number: A31362; MUID:89170129  
A:Accession: A31362  
A:Molecule type: DNA  
A:Residues: 1-267, 'M', 269-332, 'E', 334-485 <GAI>  
A:Cross-references: GB:M24686; GB:M24687; GB:M24688  
A:Note: the authors translated the codon GAA for residue 333 as Gln  
R:Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.  
J. Biol. Chem. 269, 28598-28605, 1994  
A:Title: Identification of cell type-dependent enhancer core element located in the 3'-d  
A:Reference number: I37168; MUID:95050659  
A:Accession: I37168  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-285 <NIB1>  
A:Cross-references: EMBL:X15324; MUID:g1197496; PIDN:CAA33385.1; PID:g1197497  
A:Accession: I37169  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 287-375 <NIB2>  
A:Cross-references: EMBL:X15325; MUID:g28695  
R:Kunapuli, S.P.; Benedict, C.R.; Kumar, A.  
Arch. Biochem. Biophys. 254, 642-646, 1987  
A:Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.  
A:Reference number: A60825; MUID:87212053  
A:Accession: A60825  
A:Molecule type: mRNA  
A:Residues: 32-184 <KUNI>  
R:Kunapuli, S.P.; Kumar, A.  
Circ. Res. 60, 786-790, 1987  
A:Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence of  
A:Reference number: I39462; MUID:87244745  
A:Accession: I39462  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-267, 'M', 269-338 <KUN2>  
A:Cross-references: GB:M69110; MUID:g178643; PIDN:AAA52282.1; PID:g9533181  
R:Kageyama, R.; Ohkubo, H.; Nakanishi, S.  
Biochemistry 23, 3603-3609, 1984  
A:Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequ  
A:Reference number: A90487; MUID:85000455  
A:Accession: A90487  
A:Molecule type: mRNA  
A:Residues: 1-267, 'M', 269-485 <KAG>  
A:Cross-references: GB:K02215; MUID:g178639; PIDN:AAA51731.1; PID:g178640  
A:Note: it is uncertain whether Met-1 or Met-10 is the initiator  
R:Tekksbury, D.A.; Dart, R.A.; Travis, J.  
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981  
A:Title: The amino terminal amino acid sequence of human angiotensinogen.  
A:Reference number: A90226; MUID:81255848  
A:Accession: A90226

A:Molecule type: protein  
A:Residues: 34-46, 'X', 48-50, 'S', 52-57, 'D' <TEW>  
R:Hixson, J.E.; Powers, P.K.  
Hum. Genet. 96, 110-112, 1995  
A:Title: Detection and characterization of new mutations in the human angiotensinogen  
A:Reference number: I54281; MUID:95331754  
A:Accession: I54281  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 176-241, 'I', 243-267, 'M', 269-287, 'ANLSAG' <HIX>  
A:Cross-references: GB:S78529; MUID:g999316; PIDN:AD14287.1; PID:g4261987  
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted  
e I (angiotensin-converting enzyme), primarily in the lungs.  
C:Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and  
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.  
C:Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels,  
o induces thirst.  
C:Comment: Angiotensin II and angiotensin III are equally potent in stimulating the s  
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.  
C:Genetics:  
A:Gene: GDB:AGT  
A:Cross-references: GDB:118750; OMIM:106150  
A:Map position: 1q42-lq43  
A:Introns: 286/1; 375/2; 423/3  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor  
F:1-33/Domain: (or 10-33) signal sequence #status predicted <SIG>  
F:34-485/Product: angiotensinogen #status predicted <MPT>  
F:34-43/Product: angiotensin I #status experimental <PPI>  
F:34-41/Product: angiotensin II #status experimental <PP2>  
F:35-41/Product: angiotensin III #status experimental <PP3>  
F:47,170,304,328/Binding site: carbohydrate (Asn) #status predicted  
Query Match 100.0%; Score 34; DB 1; Length 485;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYIH 6  
|||||  
Db 34 DRVYIH 39  
RESULT 8  
S72233  
transcription factor tbx6 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 14-Feb-1997 #sequence-revision 13-Mar-1997 #text-change 05-Nov-1999  
C:Accession: S72233; S72232  
R:Agulnik, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: S72233  
A:Accession: S72233  
A:Molecule type: mRNA  
A:Residues: 1-540 <AGU>  
A:Cross-references: EMBL:U57331; MUID:g1620601; PIDN:AAC53110.1; PID:g1620602  
R:Agulnik, S.I.; Garvey, N.; Hancock, S.; Ruvinsky, I.; Chapman, D.L.; Agulnik, I.; B  
Genetics 144, 249-254, 1996  
A:Title: Evolution of mouse T-box genes by tandem duplication and cluster dispersion.  
A:Reference number: S72230; MUID:97032942  
A:Accession: S72232  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 100-280 <AGW>  
A:Cross-references: EMBL:U57331  
C:Genetics:  
A:Gene: tbx6  
C:Superfamily: T-box homology  
C:Keywords: DNA binding  
F:100-282/Domain: T-box homology <TBX>  
Query Match 100.0%; Score 34; DB 2; Length 540;

Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||  
Db 170 DRVYIH 175

RESULT 9  
A06024  
angiotensin I - Japanese quail  
C:Species: Coturnix coturnix japonica (Japanese quail)  
C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-May-1999  
C:Accession: A06024  
R:Takei, Y.; Hasegawa, Y.  
Gen. Comp. Endocrinol. 79, 12-22, 1990  
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of these  
A:Reference number: A06024; MUID:90284684  
A:Accession: A06024  
A:Molecule type: protein  
A:Residues: 1-10 <TAK>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 97.1%; Score 33; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.31;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||  
Db 1 DRVYVH 6

RESULT 10  
A09017  
angiotensin precursor - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A09017; A01250  
R:Nakayama, T.; Nakajima, T.; Sokabe, H.  
Chem. Pharm. Bull. 21, 2085-2087, 1973  
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its  
A:Reference number: A09017; MUID:74127845  
A:Accession: A09017  
A:Molecule type: protein  
A:Residues: 1-10 <NAK>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <ANI>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 33; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.31;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||  
Db 1 DRVYVH 6

RESULT 11  
A09045  
angiotensin precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A09045; A01250  
R:Elliot, D.F.; Peart, W.S.  
Biochem. J. 65, 246-254, 1957  
A:Title: The amino acid sequence in a hypertensin.  
A:Reference number: A09045  
A:Accession: A09045  
A:Molecule type: protein

A:Residues: 1-10 <ELL>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <ANI>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 33; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 0.31;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||  
Db 1 DRVYVH 6

RESULT 12  
B42845  
3-hydroxybutyrate dehydrogenase (EC 1.1.1.30) - bovine (fragments)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Sep-1998  
C:Accession: B42845  
R:Marks, A.R.; McIntyre, J.O.; Duncan, T.M.; Erdjument-Bromage, H.; Tempst, P.; Fleis  
J. Biol. Chem. 267, 15459-15463, 1992  
A:Title: Molecular cloning and characterization of (R)-3-hydroxybutyrate dehydrogenas  
A:Reference number: A42845; MUID:92348395  
A:Accession: B42845  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-178 <MAR>  
A:Experimental source: heart  
A:Note: sequence extracted from NCBI backbone (NCBIP:109586, NCBIP:109588, NCBIP:1095  
C:Superfamily: retinol dehydrogenase; short-chain alcohol dehydrogenase homology  
C:Keywords: mitochondrion; oxidoreductase  
F:10-108/Domain: short-chain alcohol dehydrogenase homology (fragments) <SADH>

Query Match 97.1%; Score 33; DB 2; Length 178;  
Best Local Similarity 83.3%; Pred. No. 6.5;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||  
Db 173 DRVYIH 178

RESULT 13  
S07207  
Crinia-angiotensin, skin - frog (Crinia georgiana)  
C:Species: Crinia georgiana  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Aug-2000  
C:Accession: S07207  
R:Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.  
Experientia 35, 1132-1133, 1979  
A:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II  
A:Reference number: S07207; MUID:80024575  
A:Accession: S07207  
A:Molecule type: protein  
A:Residues: 1-11 <ERS>  
C:Superfamily: unassigned animal peptides

Query Match 94.1%; Score 32; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 0.57;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||  
Db 4 DRVYVH 9

RESULT 14  
F84339  
hypothetical protein Vng1886c [imported] - Halobacterium sp. NRC-1



C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84339  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483  
A:Accession: F84339  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-263 <STO>  
A:Cross-references: GB:AE004437; NID:gl0581327; PIDN:AAG20082.1; GSPDB:GN00138  
C:Genetics:  
A:Gene: VNG1886C

Query Match 94.1%; Score 32; DB 2; Length 263;  
Best Local Similarity 83.3%; Pred. No. 16;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
||||:|  
Db 215 DRVYILH 220

RESULT 15  
H69095  
carbon monoxide dehydrogenase, alpha subunit - Methanobacterium thermoautotrophicum (str  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C:Accession: H69095  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.  
Kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
A:Reference number: A69000; MUID:98037514  
A:Accession: H69095  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-460 <MTH>  
A:Cross-references: GB:AE000928; GB:AE000666; NID:g2622835; PIDN:AAB86182.1; PID:g262284  
C:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH1710

Query Match 94.1%; Score 32; DB 2; Length 460;  
Best Local Similarity 83.3%; Pred. No. 30;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
||||:|  
Db 262 DRVYILH 267

Search completed: July 1, 2002, 07:46:29  
Job time: 450 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:08 ; Search time 34.05 seconds  
(without alignments)  
6.823 Million cell updates/sec

Title: US-09-723-197-8  
Perfect score: 34  
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	34	100.0	8	1	ANG2_BOTJA	Q10582	bothrops ja
2	34	100.0	14	1	ANGT_HORSE	P01016	equus cabal
3	34	100.0	436	1	TBX6_HUMAN	O95947	homo sapien
4	34	100.0	476	1	ANGT_SHEEP	P20757	ovis aries
5	34	100.0	477	1	ANGT_MOUSE	P11859	mus musculus
6	34	100.0	477	1	ANGT_RAT	P01015	rattus norv
7	34	100.0	485	1	ANGT_HUMAN	P01019	homo sapien
8	34	100.0	540	1	TBX6_MOUSE	P70327	mus musculus
9	33	97.1	10	1	ANG1_BOTJA	Q10581	bothrops ja
10	33	97.1	10	1	ANGT_BOVIN	P01017	bos taurus
11	33	97.1	10	1	ANGT_CHICK	P01018	gallus gall
12	33	97.1	178	1	BDH_BOVIN	Q02337	bos taurus
13	32	94.1	11	1	ANGT_CRIGE	P09037	crinia geor
14	30	88.2	344	1	BDH_RAT	P29147	rattus norv
15	30	88.2	456	1	FRB5_MOUSE	Q64378	mus musculus
16	30	88.2	457	1	FRB5_HUMAN	P13451	homo sapien
17	30	88.2	471	1	Y872_HAEIN	O57491	haemophilus
18	30	88.2	625	1	THRB_BOVIN	P00735	bos taurus
19	30	88.2	970	1	T3RE_BPPI	P08764	bacterioph
20	30	88.2	1062	1	CERU_MOUSE	Q61147	mus musculus
21	30	88.2	1065	1	CERU_HUMAN	P00450	homo sapien
22	29	85.3	212	1	UL03_HSVB	P28942	equine herp
23	29	85.3	376	1	FA10_TROCA	P81428	tropidochis
24	29	85.3	457	1	FRB4_MOUSE	P30416	mus musculus
25	29	85.3	457	1	FRB4_RABIT	P27124	oryctolagus
26	29	85.3	458	1	FRB4_HUMAN	Q02790	homo sapien
27	29	85.3	654	1	BFR2_HUMAN	Q01742	homo sapien
28	29	85.3	659	1	POL_CERV	P05400	carnation e
29	29	85.3	801	1	FRF3_MOUSE	Q61851	mus musculus
30	29	85.3	802	1	FRF3_HUMAN	P22455	homo sapien
31	29	85.3	806	1	CEK2_CHICK	P18460	gallus gall
32	29	85.3	806	1	FRG3_HUMAN	P22607	homo sapien
33	29	85.3	808	1	FRG4_MOUSE	Q03142	mus musculus

## ALIGNMENTS

```
RESULT 1
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Bordneresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 34; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6
Db 1 DRVYIH 6

RESULT 2
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN SERPINB8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
RT polypeptide renin substrate.";
```

RL J. Exp. Med. 106:439-453(1957).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR PIR; A01250; A01250.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBD7 CRC64;  
  
Query Match 100.0%; Score 34; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DRVYIH 6  
| | | | |  
Db 1 DRVYIH 6  
  
RESULT 3  
TBX6\_HUMAN  
ID TBX6\_HUMAN STANDARD; PRT; 436 AA.  
AC O95947;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX6 (T-box protein 6).  
GN TBX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=99134303; PubMed=9933572;  
RA Papapetrou C., Putt W., Fox M., Edwards Y.H.;  
RT "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";  
RL Genomics 55:238-241(1999).  
[2]  
RN SEQUENCE OF 135-272 FROM N.A.  
RP TISSUE=Myeloid;  
RC MEDLINE=99107806; PubMed=9888994;  
RX Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,  
RA Armstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;  
RT "Identification, mapping and phylogenomic analysis of four new human  
RT members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";  
RL Genomics 55:10-20(1999).  
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN  
CC DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF  
CC PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).  
CC -1- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).  
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL  
CC TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT  
CC TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A  
CC SECOND PHASE IN SOME ADULT TISSUES.  
CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
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DR EMBL; AJ007989; CAA07812.1; -;  
DR EMBL; AJ010279; CAB37938.1; -;  
DR HSP; P24781; IXHR.  
DR MIM; 602427; -;  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein;  
KW Developmental protein.  
FT DNA\_BIND 100 273 T-BOX.  
FT CONFLICT 207 207 H -> HV (IN REF. 2).  
SQ SEQUENCE 436 AA; 47017 MW; 438178BD31B966E9 CRC64;  
  
Query Match 100.0%; Score 34; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DRVYIH 6  
| | | | |  
Db 170 DRVYIH 175  
  
RESULT 4  
ANGT\_SHEEP  
ID ANGT\_SHEEP STANDARD; PRT; 476 AA.  
AC P20757;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPINAG OR AGT.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=95072318; PubMed=7765514;  
RX Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,  
RA Murakami K., Nakamura Y.;  
RT "Sequencing and expression of sheep angiotensinogen cDNA.";  
RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).  
[2]  
RN SEQUENCE OF 25-39.  
RP MEDLINE=86136099; PubMed=3081342;  
RX Fernley R.T., John M., Niall H.D., Coghlan J.P.;  
RT "Purification and characterization of ovine angiotensinogen.";  
RL Eur. J. Biochem. 154:597-601(1986).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
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CC -----
CC EMBL; D17520; BAA04470.1; -.
CC PIR; A25406; A25406.
CC InterPro; IPR000227; Angiotensngn.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC PRINTS; PR00654; ANGIOTENSNGN.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; Plasma; Serpin; Signal.
CC Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
CC CHAIN 1 24
CC PEPTIDE 25 476 ANGIOTENSINOGEN.
CC PEPTIDE 25 34 ANGIOTENSIN I.
CC PEPTIDE 25 32 ANGIOTENSIN II.
CC CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 476 AA; 51304 MW; CBA517CD9FA029F7 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.1; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 DRVYIH 6
Db 25 DRVYIH 30

RESULT 5
ANGT_MOUSE STANDARD; PRT; 477 AA.
AC P11859;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN SERPINA8 OR AGT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88284703; PubMed=3397061;
RA Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RL Genomics 2:240-248(1988).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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CC EMBL; AF045886; AAC01765.1; JOINED.
CC EMBL; AF045885; AAC01765.1; JOINED.
CC EMBL; AF045884; AAC01765.1; JOINED.
CC PIR; A29978; A29978.
CC MGD; MGI:87963; Agt.
CC InterPro; IPR000227; Angiotensngn.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.

DR PRINTS; PR00654; ANGIOTENSNGN.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; FALSE_NEG.
DR Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
DR SIGNAL 1 24
DR CHAIN 25 477 ANGIOTENSINOGEN.
DR PEPTIDE 25 34 ANGIOTENSIN I.
DR PEPTIDE 25 32 ANGIOTENSIN II.
DR CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
DR CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
DR CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
DR SEQUENCE 477 AA; 51990 MW; A877F4029F338607 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.2; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 DRVYIH 6
Db 25 DRVYIH 30

RESULT 6
ANGT_RAT STANDARD; PRT; 477 AA.
AC P01015;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN SERPINA8 OR AGT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WISTAR.
RX MEDLINE=83169849; PubMed=6572971;
RA Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA Nakanishi S.;
RT "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN [2]
RP SEQUENCE OF 25-34.
RX MEDLINE=73060322; PubMed=4344907;
RA Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. II. Structure of rat
RT angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 20:1579-1581(1972).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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DR InterPro; IPR000227; Angiotensnngn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; FALSE\_NEG.  
KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 477 ANGIOTENSINOGN.  
FT PEPTIDE 25 34 ANGIOTENSIN I.  
FT PEPTIDE 25 32 ANGIOTENSIN II.  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 477 AA; 51981 MW; 689051A5788D693D CRC64;

Query Match 100.0%; Score 34; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
|||||  
Db 25 DRVYIH 30

RESULT 7  
ANGT\_HUMAN  
ID ANGT\_HUMAN STANDARD; PRT; 485 AA.  
AC P01019; Q16358; Q16359;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPINA8 OR AGT  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 1  
RS SEQUENCE FROM N.A.  
RX MEDLINE=89170129; PubMed=2924688;  
RA Gaillard I., Clauser E., Corvol P.;  
RT "Structure of human angiotensinogen gene.";  
RL DNA 8:87-99(1989).  
RN 2  
RS SEQUENCE FROM N.A.  
RX MEDLINE=85000455; PubMed=6089875;  
RA Kagayama R., Ohkubo H., Nakanishi S.;  
RT "Primary structure of human preangiotensinogen deduced from the  
RT cloned cDNA sequence.";  
RL Biochemistry 23:3603-3609(1984).  
RN 3  
RS SEQUENCE FROM N.A.  
RX MEDLINE=90237063; PubMed=1692023;  
RA Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,  
RA Murakami K.;  
RT "Structure and expression of the human angiotensinogen gene.  
RT Identification of a unique and highly active promoter.";  
RL J. Biol. Chem. 265:7576-7582(1990).  
RN 4  
RS SEQUENCE OF 1-338 FROM N.A.  
RX MEDLINE=87244745; PubMed=2885106;  
RA Kunapuli S.P., Kumar A.;  
RT "Molecular cloning of human angiotensinogen cDNA and evidence for the  
RT presence of its mRNA in rat heart.";  
RL Circ. Res. 60:786-790(1987).  
RN 5  
RS SEQUENCE OF 34-45, AND SUBUNITS.  
RX TISSUE-Serum;  
RC MEDLINE=95293954; PubMed=7539791;  
RA Ovig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,  
RA Stigbrand T., Gleich G.J., Sottrup-Jensen L.;  
RT "Identification of angiotensinogen and complement C3dg as novel

RT proteins binding the proform of eosinophil major basic protein in  
RT human pregnancy serum and plasma.";  
RL J. Biol. Chem. 270:13645-13651(1995).  
RN 6  
RS SEQUENCE OF 34-43.  
RX MEDLINE=69014170; PubMed=4300938;  
RA Arakawa K., Minohara A., Yamada J., Nakamura M.;  
RT "Enzymatic degradation and electrophoresis of human angiotensin I.";  
RL Biochim. Biophys. Acta 168:106-112(1968).  
RN 7  
RS STRUCTURE BY NMR OF ANGIOTENSIN II.  
RX MEDLINE=98151281; PubMed=9492317;  
RA Carpenter K.A., Wilkes B.C., Schiller P.W.;  
RT "The octapeptide angiotensin II adopts a well-defined structure in a  
RT phospholipid environment.";  
RL Eur. J. Biochem. 251:448-453(1998).  
RN 8  
RS VARIANTS MET-207; THR-268 AND CYS-281.  
RX MEDLINE=93008239; PubMed=1394429;  
RA Jeunenaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,  
RA Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,  
RA Lalouel J.-M., Corvol P.;  
RT "Molecular basis of human hypertension: role of angiotensinogen.";  
RL Cell 71:169-180(1992).  
RN 9  
RS VARIANT THR-268.  
RX MEDLINE=93291876; PubMed=8513325;  
RA Ward K., Hata A., Jeunenaitre X., Helin C., Nelson L., Namikawa C.,  
RA Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,  
RA Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;  
RT "A molecular variant of angiotensinogen associated with  
RL Nat. Genet. 4:59-61(1993).  
RN 10  
RS VARIANTS ILE-242; ARG-244 AND CYS-281.  
RX MEDLINE=95331754; PubMed=7607642;  
RA Hixson J.E., Powers P.K.;  
RT "Detection and characterization of new mutations in the human  
RL angiotensinogen gene (AGT).";  
CC Hum. Genet. 96:110-112(1995).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2  
CC heterotetramer with the proform of PRG2 and as a complex (probably  
CC a 2:2:2 heterohexamer) with pro-PRG2 and C3dg.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO  
CC ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION  
CC (PIH) (PREECLAMPSIA).  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.  
CC  
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CC  
CC EMBL; K02215; AAA51731.1; -  
DR EMBL; M24689; AAA51679.1; -  
DR EMBL; M24686; AAA51679.1; JOINED.  
DR EMBL; M24687; AAA51679.1; JOINED.  
DR EMBL; M24688; AAA51679.1; JOINED.  
DR EMBL; X15324; CAA33385.1; -  
DR EMBL; X15325; CAA33385.1; JOINED.  
DR EMBL; X15326; CAA33385.1; JOINED.  
DR EMBL; X15327; CAA33385.1; JOINED.  
DR

DR EMBL; M691110; AAA52282.1; -;  
DR EMBL; S78529; AAD14287.1; -;  
DR EMBL; S78530; AAD14288.1; -;  
DR PIR; A01249; ANHU.  
DR PIR; A31362; A31362.  
DR PIR; A35203; A35203.  
DR SWISS-2DPAGE; P01019; HUMAN.  
DR MIM; 106150; -;  
DR InterPro; IPR000227; Angiotensin.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Vasconstrictor; Glycoprotein; Plasma; Serpin; Signal;  
KW Disease mutation; Polymorphism.  
FT SIGNAL 1 33  
FT CHAIN 34 485 ANGIOTENSINOGEN.  
FT PEPTIDE 34 43 ANGIOTENSIN I.  
FT PEPTIDE 34 41 ANGIOTENSIN II.  
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 207 207 T -> M.  
FT VARIANT 242 242 /FTID-VAR\_007093.  
FT VARIANT 244 244 T -> I (IN HYPERTENSION).  
FT VARIANT 244 244 /FTID-VAR\_007094.  
FT VARIANT 268 268 L -> R (IN HYPERTENSION).  
FT VARIANT 268 268 /FTID-VAR\_007095.  
FT VARIANT 281 281 M -> T (IN HYPERTENSION).  
FT VARIANT 281 281 /FTID-VAR\_007096.  
FT VARIANT 333 333 Y -> C (IN HYPERTENSION).  
FT CONFLICT 333 333 Q -> E (IN REF. 1).  
FT SEQUENCE 485 AA; 53154 MW; 5026C2DFB2D236E CRC64;  
  
Query Match 100.0%; Score 34; DB 1; Length 485;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVYIH 6  
Db 34 DRVYIH 39  
IIIIII  
  
RESULT 8  
TBX6.MOUSE STANDARD; PRT; 540 AA.  
AC P70327;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX6 (T-box protein 6).  
GN TBX6  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=97032942; PubMed=8878690;  
RA Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,  
RA Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;  
RT "Evolution of mouse T-box genes by tandem duplication and cluster  
dispersion".  
RT Genetics 144:249-254 (1996).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Gastrula;  
RC MEDLINE=97115702; PubMed=8954725;  
RX

RA Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;  
RT "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at  
gastrulation.";  
RL Dev. Biol. 180:534-542 (1996).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=98140705; PubMed=9490412;  
RA Chapman D.L., Papaioannou V.E.;  
RT "Three neural tubes in mouse embryos with mutations in the T-box gene  
Tbx6.";  
RL Nature 391:695-697 (1998).  
CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN  
DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL  
MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS  
DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL  
PATHWAY.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION  
STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL  
MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,  
PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK  
AS THE SOURCE OF MESODERM.  
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
  
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EMBL; U57331; AAC53110.1; -;  
DR HSSP; P24781; IXHR.  
DR MGD; MGI:102539; Tbx6.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein;  
KW Developmental protein.  
FT DOMAIN 61 64 POLY-ALA.  
FT DOMAIN 79 82 POLY-PRO.  
FT DNA\_BIND 100 273 T-BOX.  
FT SEQUENCE 540 AA; 58628 MW; BC834CE2745E8561 CRC64;  
  
Query Match 100.0%; Score 34; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVYIH 6  
Db 170 DRVYIH 175  
IIIIII  
  
RESULT 9  
ANG1.BOTJA STANDARD; PRT; 10 AA.  
ID ANGL\_BOTJA  
AC Q10581;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide I (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodactylia; Squamata; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]

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RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 10
FT SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6
Db 1 DRVYVH 6

RESULT 10
ANGT_BOVIN
ID ANGT_BOVIN STANDARD; PRT; 10 AA.
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
CN SERPINAB OR AGT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin.";
RL Biochem. J. 65:246-254(1957).
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A01250; A01250.
DR PIR; A0345; A0345.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6
Db 1 DRVYVH 6

RESULT 11
ANGT_CHICK

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ID ANGT_CHICK STANDARD; PRT; 10 AA.
AC P01018;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
CN SERPINAB OR AGT.
OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE.
RC SPECIES=Chicken;
RX MEDLINE=74127845; PubMed=4361802;
RA Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
RT angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.c.japonica;
RX MEDLINE=90284684; PubMed=2191893;
RA Takei Y., Hasegawa Y.;
RT "Vasopressor and depressor effects of native angiotensins and
RT inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol. 79:12-22(1990).
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A01250; A01250.
DR PIR; A0917; A0917.
DR PIR; A0624; A0624.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1232 MW; CEEFBDD761F2DB42 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6
Db 1 DRVYVH 6

RESULT 12
BDH_BOVIN
ID BDH_BOVIN STANDARD; PRT; 178 AA.
AC Q02337;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH)
DE (3-hydroxybutyrate dehydrogenase) (Fragments).
GN BDH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

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Best Local Similarity 66.7%; Pred. No. 36;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|:|:|:  
Db 51 DKVYVH 56

Search completed: July 1, 2002, 07:47:09  
Job time: 475 sec

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RESULT 15
FKB5_MOUSE
ID FKB5_MOUSE STANDARD; PRT; 456 AA.
AC O64378;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl cis-trans
DE isomerase) (EC 5.2.1.8) (PPIase) (Rotamase).
GN FKBP5 OR FKBP51.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96074651; PubMed=7479941;
RA Yeh W.-C., Li T.-K., Bierer B.E., McKnight S.L.;
RT "Identification and characterization of an immunophilin expressed
RT during the clonal expansion phase of adipocyte differentiation.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11081-11085(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=Thymus;
RX MEDLINE=95349606; PubMed=7542743;
RA Baughman G., Wiederrecht G.J., Campbell N.F., Martin M.M.,
RA Bourgeois S.;
RT "FKBP51, a novel T-cell-specific immunophilin capable of calcineurin
RT inhibition.";
RL Mol. Cell. Biol. 15:4395-4402(1995).
CC -!- FUNCTION: INTERACTS WITH PROGESTERONE RECEPTOR (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, HIGHEST LEVELS FOUND IN THE
CC LIVER, SKELETAL MUSCLE, KIDNEY AND THYMUS. EXPRESSION IS REGULATED
CC DURING ADIPOCYTE DIFFERENTIATION.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2
CC FKBP-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U36220; AAA89162.1; -
DR EMBL; U16959; AAA86983.1; -
DR HSSP; P27124; IROT.
DR MGD; MGI:104670; Fkbp5.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 2.
DR Pfam; PF00515; TPR; 3.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS00509; FKBP_PPIASE_3; 2.
KW Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
FT DOMAIN 50 138 PPIASE, FKBP-TYPE 1.
FT DOMAIN 165 251 PPIASE, FKBP-TYPE 2.
FT REPEAT 268 301 TPR 1.
FT REPEAT 317 350 TPR 2.
FT REPEAT 352 384 TPR 3.
SQ SEQUENCE 456 AA; 50966 MW; 8FD0C9B61478EB46 CRC64;
```

Query Match 88.2%; Score 30; DB 1; Length 456;

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:12 ; Search time 122.73 Seconds  
(without alignments)  
8.457 Million cell updates/sec

Title: US-09-723-197-8  
Perfect score: 34  
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL19:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	14	5 Q10757	Q10757 theromyzon
2	34	100.0	245	6 Q95J13	Q95J13 pan troglod
3	34	100.0	295	4 Q9HA44	Q9HA44 homo sapien
4	34	100.0	461	11 Q9D2V0	Q9D2V0 mus musculu
5	34	100.0	477	4 Q96FD5	Q96FD5 homo sapien
6	34	100.0	485	4 Q96F91	Q96F91 homo sapien
7	34	100.0	485	6 Q9GLP7	Q9GLP7 pan troglod
8	34	100.0	485	6 Q9GLP6	Q9GLP6 gorilla gor
9	34	100.0	485	6 Q9GLN8	Q9GLN8 pan troglod
10	34	100.0	486	6 Q9TSZ0	Q9TSZ0 callithrix
11	33	97.1	10	13 Q9PS07	Q9PS07 alligator m
12	33	97.1	457	6 Q9XSH5	Q9XSH5 saimiri bol
13	32	94.1	263	17 Q9HNV8	Q9HNV8 halobacteri
14	32	94.1	460	17 Q27745	Q27745 methanother
15	32	94.1	546	12 Q9LHA5	Q9LHA5 rinderpest
16	32	94.1	808	1 Q52045	Q52045 halobacteri

17	31	91.2	171	17	Q971G2	Q971G2 sulfolobus
18	31	91.2	363	16	Q9JXJ6	Q9JXJ6 neisseria m
19	30	88.2	116	2	O58039	O58039 rhodobacter
20	30	88.2	247	16	Q988V3	Q988V3 rhizobium l
21	30	88.2	388	5	Q9N508	Q9N508 caenorhabdi
22	30	88.2	388	5	Q9NAL0	Q9NAL0 caenorhabdi
23	30	88.2	420	10	Q94E08	Q94E08 oryza sativ
24	30	88.2	457	6	Q9XT11	Q9XT11 aotus nancy
25	30	88.2	457	6	Q9XS12	Q9XS12 saguinus oe
26	30	88.2	457	6	Q9SL05	Q9SL05 ceropitheci
27	30	88.2	473	2	Q9AIX7	Q9AIX7 azoarcus ev
28	30	88.2	500	5	Q18475	Q18475 caenorhabdi
29	30	88.2	510	16	Q9K716	Q9K716 bacillus ha
30	30	88.2	986	5	Q9N9W3	Q9N9W3 haemochus
31	30	88.2	1014	5	Q17505	Q17505 caenorhabdi
32	30	88.2	1048	6	Q9XT27	Q9XT27 ovis aries
33	30	88.2	1590	5	Q9V7E3	Q9V7E3 drosophila
34	29	85.3	56	13	Q91995	Q91995 xenopus lae
35	29	85.3	57	13	Q08556	Q08556 phasianidae
36	29	85.3	68	13	Q9Y121	Q9Y121 gallus gall
37	29	85.3	111	16	Q915S2	Q915S2 pseudomonas
38	29	85.3	129	11	Q63000	Q63000 rattus norv
39	29	85.3	153	2	O86161	O86161 campylobact
40	29	85.3	157	6	Q28332	Q28332 callithrix
41	29	85.3	157	6	Q28111	Q28111 bos taurus
42	29	85.3	164	2	Q9R6J1	Q9R6J1 agrobacteri
43	29	85.3	209	13	Q9DE16	Q9DE16 brachydanio
44	29	85.3	211	12	Q39300	Q39300 equine herp
45	29	85.3	216	2	Q9XA67	Q9XA67 streptomyce

ALIGNMENTS

RESULT 1

Q10757

ID Q10757 PRELIMINARY; PRT; 14 AA.

AC Q10757;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE ANGIOTENSINOGEN (FRAGMENT).

OS Theromyzon tessulatum (leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Rhynchobdellida; Glossiphoniidae; Theromyzon.

OX NCBI\_TaxID=13286;

RN [1]

RP SEQUENCE.

RX MEDLINE=95365039; PubMed=7637887;

RA Laurent V., Bulet P., Salzet M.A.;

RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like

RT molecule with forms of vertebrate angiotensinogens: a hormonal system

RT conserved in the course of evolution.";

RL Neurosci. Lett. 190:175-178(1995).

RN [2]

RP SEQUENCE OF 1-10.

RC TISSUE=BRAIN;

RX MEDLINE=96201949; PubMed=8612806;

RA Laurent V., Salzet M.;

RT "Metabolism of angiotensins by head membranes of the leech Theromyzon

RT tessulatum.";

RL FEBS Lett. 384:123-127(1996).

CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.

KW Glycoprotein; Serpin.

FT NON\_TER 14 14

SQ SEQUENCE 14 AA: 1763 MW: 335109D8EEFFBDD7 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6

Db 1 DRVYIH 6  
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RESULT 2 PRELIMINARY; PRT: 245 AA.  
Q95J13  
AC Q95J13  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN (FRAGMENT).  
GN REN.

OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=504, AND 505;

RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB062027; BAB55856.1;  
DR EMBL; AB062028; BAB55857.1;  
FT NON\_TER 245  
SQ SEQUENCE 245 AA; 26317 MW; E0092390B9803E0B CRC64;

Query Match 100.0%; Score 34; DB 6; Length 245;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||

Db 34 DRVYIH 39

RESULT 3 PRELIMINARY; PRT: 295 AA.  
Q9HA44  
ID Q9HA44  
AC Q9HA44;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CDNA FLJ1268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS TRANSCRIPTION FACTOR TBX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY GLAND;  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Watanabe S., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK022330; BAB14014.1;  
DR HSSP; P24781; 1XBR.

DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.

DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.

DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS50252; TBOX\_3; 1.

SQ SEQUENCE 295 AA; 33197 MW; F2BD3E53E0ED21E0 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 295;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||

Db 170 DRVYIH 175

RESULT 4 PRELIMINARY; PRT: 461 AA.  
Q9D2V0  
ID Q9D2V0  
AC Q9D2V0;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN.  
GN AGT.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;  
RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Karim M., Lee N.H.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Mombaerts P.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AK018763; BAB31393.1;  
DR MGD; MGI:87963; Agt.

DR InterPro; IPR000227; Angiotensin.

DR InterPro; IPR000215; Serpin.

DR PRINTS; PR00654; ANGIOTENSIN.

DR SMART; SM00093; SERPIN; 1.

SQ SEQUENCE 461 AA; 50327 MW; 446EB0881079251F CRC64;

Query Match 100.0%; Score 34; DB 11; Length 461;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIH 6  
|||||

Db 30 DRVYIH 35

RESULT 5 PRELIMINARY; PRT: 477 AA.  
Q96FD5  
ID Q96FD5  
AC Q96FD5;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE SIMILAR TO ANGIOTENSINOGEN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN, AND GLOBLASTOMA WITH EGFR AMPLIFICATION;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011231; AAH11231.1; --  
SQ SEQUENCE 477 AA; 51985 MW; AB7988B70592FDE2 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 477;

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
Db 25 DRVYIH 30  
|||||

RESULT 6  
Q96F91 PRELIMINARY; PRT; 485 AA.  
ID AC Q96F91;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN (SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE A (ALPHA-1 ANTITRYPSIN, MEMBER 8).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN, AND GLOBLASTOMA WITH EGFR AMPLIFICATION;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011519; AAH11519.1; --  
SQ SEQUENCE 485 AA; 53114 MW; 50BA5E9DCD4C8E7F CRC64;

Query Match 100.0%; Score 34; DB 4; Length 485;

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
Db 34 DRVYIH 39  
|||||

RESULT 7  
Q9GLP7 PRELIMINARY; PRT; 485 AA.  
ID AC Q9GLP7;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN.  
GN AGT.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shattuck-Eidens D., McGrail M., Stone S.;  
RT "Germline mutations in the angiotensinogen gene cause predisposition to type 1 diabetes mellitus."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AF188487; AAG29056.1; --  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Serpin.  
SQ SEQUENCE 485 AA; 53140 MW; 49EFB54AF31F8ADC CRC64;

Query Match 100.0%; Score 34; DB 6; Length 485;

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
Db 34 DRVYIH 39  
|||||

RESULT 8  
Q9GLP6 PRELIMINARY; PRT; 485 AA.  
ID AC Q9GLP6;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN.  
GN AGT.  
OS Gorilla gorilla (gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
OX NCBI\_TaxID=9593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shattuck-Eidens D., McGrail M., Stone S.;  
RT "Germline mutations in the angiotensinogen gene cause predisposition to type 1 diabetes mellitus."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AF188488; AAG29057.1; --  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Serpin.  
SQ SEQUENCE 485 AA; 53186 MW; 53BC9235271C8255 CRC64;

Query Match 100.0%; Score 34; DB 6; Length 485;

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
Db 34 DRVYIH 39  
|||||

RESULT 9  
Q9GLN8 PRELIMINARY; PRT; 485 AA.  
ID AC Q9GLN8;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN.  
GN AGT.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20469400; PubMed=11013071;  
RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,  
RA Jeunemaitre X.;  
RT "Human-Chimpanzee DNA sequence variation in the four major genes of  
RT the renin-angiotensin system.";  
RL Genomics 69:14-26(2000).  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AF193461; AAG30306.1; -.  
DR EMBL; AF193458; AAG30306.1; JOINED.  
DR EMBL; AF193459; AAG30306.1; JOINED.  
DR EMBL; AF193460; AAG30306.1; JOINED.  
DR InterPro; IPR000227; Angiotensin.  
DR InterPro; IPR000215; Serpin.  
DR PRINTS; PR00654; Angiotensin.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Serpin.  
SQ SEQUENCE 485 AA; 53110 MW; C14C67E49A53F05F CRC64;

Query Match 100.0%; Score 34; DB 6; Length 485;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYIH 6  
DB 34 DRVYIH 39

RESULT 10  
Q9TSZ0 PRELIMINARY; PRT; 486 AA.  
AC Q9TSZ0;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN PRECURSOR.  
GN ANGT.  
OS Callithrix jacchus (Common marmoset).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
OX NCBI\_TaxID=9483;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20065005; PubMed=10598135;  
RA Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;  
RT "Cloning and characterization of marmoset renin: comparison with human  
RT renin.";  
RL J. Cardiovasc. Pharmacol. 34:893-897(1999).  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AJ132343; CAB64880.1; -.  
DR InterPro; IPR000227; Angiotensin.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSIN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
KW Serpin; Signal.  
FT SIGNAL 1 33 POTENTIAL.  
FT CHAIN 34 486 ANGIOTENSINOGEN.  
SQ SEQUENCE 486 AA; 53374 MW; 5408129B271FB8B CRC64;

Query Match 100.0%; Score 34; DB 6; Length 486;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYIH 6  
DB 34 DRVYIH 39

RESULT 11  
Q9PS07 PRELIMINARY; PRT; 10 AA.  
AC Q9PS07;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE ANGIOTENSIN I, ANG I.  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93307610; PubMed=8319878;  
RA Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,  
RA Stephens G.A., Sakakibara S.;  
RT "New angiotensin I isolated from a reptile, Alligator  
RT mississippiensis.";  
RL Gen. Comp. Endocrinol. 90:214-219(1993).  
SQ SEQUENCE 10 AA; 1216 MW; CEE38DD761F2DB42 CRC64;

Query Match 97.1%; Score 33; DB 13; Length 10;  
Best Local Similarity 83.3%; Pred. No. 66;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYIH 6  
DB 1 DRVYIH 6

RESULT 12  
Q9XSH5 PRELIMINARY; PRT; 457 AA.  
AC Q9XSH5;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE FK506-BINDING PROTEIN FKBP51.  
OS Saimiri boliviensis (Bolivian squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.  
OX NCBI\_TaxID=27679;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20539274; PubMed=11089542;  
RA Denny W.B., Valentine D.L., Reynolds P.D., Smith D.F., Scammell J.G.;  
RT "Squirrel Monkey Immunophilin FKBP51 Is a Potent Inhibitor of  
RT Glucocorticoid Receptor Binding.";  
RL Endocrinology 141:4107-4113(2000).  
DR EMBL; AF140759; AAD32678.1; -.  
DR HSP; P27124; IROT.  
DR InterPro; IPR001179; FKBP\_PPIase.  
DR InterPro; IPR001440; TPR.  
DR Pfam; PF00254; FKBP; 2.  
DR Pfam; PF00515; TPR; 2.  
DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
DR PROSITE; PS0059; FKBP\_PPIASE\_3; 2.  
SQ SEQUENCE 457 AA; 51169 MW; DFF9E1D81F7759A8 CRC64;

Query Match 97.1%; Score 33; DB 6; Length 457;  
Best Local Similarity 83.3%; Pred. No. 33;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYIH 6  
DB 51 DRVYIH 56

RESULT 13



Q9HNY8  
ID Q9HNY8 PRELIMINARY; PRT; 263 AA.  
AC Q9HNY8;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE VNG1886C.  
GN VNG1886C.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;  
OC Halobacterium.  
OX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20504483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weiti R., Goo Y.A.,  
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Madocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebbhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;  
RT "Genome sequence of Halobacterium species NRC-1";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL; AE005087; AAG20082.1;  
DR InterPro: IPR002831; DUF118.  
DR Pfam; PF01978; DUF118; 1.  
DR ProDom; PD008327; DUF118; 1.  
KW Complete proteome.  
SQ SEQUENCE 263 AA; 29005 MW; 22EB839F64CE8542 CRC64;

Query Match 94.1%; Score 32; DB 17; Length 263;  
Best Local Similarity 83.3%; Pred. No. 31;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
||||:|  
Db 215 DRVYLH 220

RESULT 14  
O27745 PRELIMINARY; PRT; 460 AA.  
AC O27745;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE CARBON MONOXIDE DEHYDROGENASE, ALPHA SUBUNIT.  
GN MTH1710.  
OS Methanothermobacter thermoautotrophicus.  
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;  
OC Methanothermobacter.  
OX NCBI\_TaxID=145262;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DELTA H;  
RX MEDLINE=98037514; PubMed=9371463;  
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,  
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
deltaH: functional analysis and comparative genomics.";  
RL J. Bacteriol. 179:7135-7155(1997).  
DR EMBL; AE000928; AAB86182.1;  
KW Complete proteome.  
SQ SEQUENCE 460 AA; 51737 MW; DB4D50693D154BDA CRC64;

Query Match 94.1%; Score 32; DB 17; Length 460;  
Best Local Similarity 83.3%; Pred. No. 56;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
||||:|  
Db 262 DRVYLH 267

RESULT 15  
Q91HA5 PRELIMINARY; PRT; 546 AA.  
AC Q91HA5;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE FUSION PROTEIN.  
GN F.  
OS Rinderpest virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OX NCBI\_TaxID=11241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K;  
RX MEDLINE=21014265; PubMed=11186456;  
RA Aianot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,  
RA Gusev A.A.;  
RT "Primary structure of the F-gene from Rinderpest virus strain K.";  
RL Mol. Gen. Mikrobiol. Virusol. 4:29-33(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K;  
RA Ayanot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,  
RA Gusev A.A.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY035887; AAKG3190.1;  
SQ SEQUENCE 546 AA; 58572 MW; 449B2B2DD7405F0B CRC64;

Query Match 94.1%; Score 32; DB 12; Length 546;  
Best Local Similarity 83.3%; Pred. No. 66;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6  
||||:|  
Db 435 DRVYLH 440

Search completed: July 1, 2002, 07:45:13  
Job time: 409 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 seconds

(without alignments)  
3.509 Million cell updates/sec

Title: US-09-723-197-9

Perfect score: 26

Sequence: 1 DRVYI 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_032802: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	26	100.0	5	17	AAR95670	Angiotensin II fra
2	26	100.0	5	19	AAW64736	Angiotensin II pep
3	26	100.0	5	19	AAW65605	Angiotensin II ana
4	26	100.0	5	19	AAW71118	Peptide AII(1-5) u
5	26	100.0	5	20	AAW49594	Angiotensin analog
6	26	100.0	5	20	AAW33909	Angiotensin II ana
7	26	100.0	5	20	AAW30547	Amino acid sequenc
8	26	100.0	5	20	AAW30591	Amino acid sequenc
9	26	100.0	5	20	AAW32722	Angiotensin II ana
10	26	100.0	5	20	AAW33776	Angiotensin II (AI
11	26	100.0	5	20	AAW15353	Angiotensin II (AI

12	26	100.0	5	20	AAW15313	Angiotensin II (AI
13	26	100.0	5	21	AAW27409	Angiotensin II ana
14	26	100.0	5	21	AAW28107	Angiotensin II ana
15	26	100.0	5	21	AAW84568	Amino acid sequenc
16	26	100.0	5	21	AAW84132	Peptide comprising
17	26	100.0	5	21	AAW77045	Angiotensin II (AI
18	26	100.0	5	21	AAW57409	Angiotensin peptid
19	26	100.0	5	22	AAE08879	AII peptide (resid
20	26	100.0	5	22	AAE02996	Human angiotensin
21	26	100.0	5	22	AAE03159	Human angiotensin
22	26	100.0	5	22	AAW60413	C-terminally trunc
23	26	100.0	6	17	AAW95669	Angiotensin II fra
24	26	100.0	6	19	AAW65604	Angiotensin II ana
25	26	100.0	6	19	AAW64735	Angiotensin II pep
26	26	100.0	6	19	AAW71117	Peptide AII(1-6) u
27	26	100.0	6	20	AAW49593	Angiotensin analog
28	26	100.0	6	20	AAW33908	Angiotensin II ana
29	26	100.0	6	20	AAW30546	Amino acid sequenc
30	26	100.0	6	20	AAW30590	Amino acid sequenc
31	26	100.0	6	20	AAW32721	Angiotensin II ana
32	26	100.0	6	20	AAW33775	Angiotensin II (AI
33	26	100.0	6	20	AAW15352	Angiotensin II (AI
34	26	100.0	6	20	AAW15312	Angiotensin II (AI
35	26	100.0	6	21	AAW27408	Angiotensin II ana
36	26	100.0	6	21	AAW28106	Angiotensin II ana
37	26	100.0	6	21	AAW84131	Peptide comprising
38	26	100.0	6	21	AAW77044	Angiotensin II (AI
39	26	100.0	6	21	AAW57408	Angiotensin peptid
40	26	100.0	6	22	AAE08878	AII peptide (resid
41	26	100.0	6	22	AAE02995	Human angiotensin
42	26	100.0	6	22	AAE03158	Human angiotensin
43	26	100.0	7	17	AAW95665	Angiotensin II fra
44	26	100.0	7	19	AAW65600	Angiotensin II ana
45	26	100.0	7	19	AAW64731	Angiotensin II pep

ALIGNMENTS

RESULT 1

AAR95670

ID AAR95670 standard; peptide; 5 AA.

XX AAR95670;

XX 09-JAN-1997 (first entry)

XX Angiotensin II fragment AII(1-5).

XX Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;  
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;  
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.

XX Synthetic.

XX WO9614858-A1.

XX 23-MAY-1996.

XX 14-NOV-1995; 95WO-US14764.

XX 06-JUN-1995; 95US-0465775.

XX 14-NOV-1994; 94US-0337781.

XX (UVSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega GS, Rodgers K;

XX WPI; 1996-259561/26.

XX Accelerating wound healing by application of angiotensin II  
PT fragments - are effective at very low concn. and do not cause  
PT hypertension

XX PS Disclosure: Page 4; 46pp; English.

XX CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see

XX CC AAR95662) is an octapeptide present in humans and other species. AT2 is

CC CC one of the most potent vasoconstrictors known, causing constriction of

CC CC the arterioles. The formation of angiotensin is initiated by the action

CC CC of renin on angiotensinogen. The substance formed is a decapeptide

CC CC called angiotensin I which is converted by the enzyme angiotensinase (by

CC CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release

CC CC of extracellular matrices involved in wound repair. These fragments can

CC CC be used in a compound for accelerating wound healing. The compounds are

CC CC administered as matricial or micellar solutions, formulated with a

CC CC carrier or diluent, alternatively the compound is applied in conjunction

CC CC with a wound dressing. The carrier used in the composition is

CC CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly

CC CC glycols. By using fragments of this sequence (or analogues of it),

CC CC growth as well as healing of tissues is improved, such as in cases of

CC CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or

CC CC intraperitoneal surgical wounds. The compounds containing the AT2

CC CC fragments are less hypertensive than full length AT2, and are also

CC CC effective at much lower (nanomolar) concentrations than full length AT2.

XX CC Sequence 5 AA;

SQ Query Match 100.0%; Score 26; DB 17; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

DB 1 drvyi 5

RESULT 2

AAW64736

ID AAW64736 standard; peptide; 5 AA.

XX AC AAW64736;

XX AC AAW64736;

DT 02-NOV-1998 (first entry)

XX DE Angiotensin II peptide #8.

XX KW Proliferation; mesenchymal stem cell; lineage-specific cell;

XX KW haematopoietic; cell culture; transplantation; treatment; malignant;

XX KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.

XX OS Synthetic.

OS Homo sapiens.

XX WO9832457-A2.

XX PN 30-JUL-1998.

XX PF 26-JAN-1998; 98WO-US01552.

XX PR 23-JAN-1998; 98US-0066593.

XX PR 28-JAN-1997; 97US-0036507.

XX PR 08-MAY-1997; 97US-0046859.

XX PR 28-OCT-1997; 97US-0063684.

XX PR 31-OCT-1997; 97US-0063910.

XX PR 18-NOV-1997; 97US-0065612.

XX PR 26-NOV-1997; 97US-0066593.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI dizerega G, Rodgers KE;

XX DR WPI; 1998-437044/37.

XX PT Promoting haematopoietic and mesenchymal cell proliferation and

PT differentiation - by contacting the cells with angiotensinogen,

XX angiotensin I or II, or analogues or fragments of these

XX PS Claim 7; Page 14; 114pp; English.

XX CC AAW64728-W64763 are peptides used in a novel method for accelerating the

CC CC proliferation of mesenchymal stem cells (MSCs), haematopoietic

CC CC lineage-specific cells or mesenchymal lineage-specific cells. The method

CC CC involves contacting the cells with an active agent comprising a sequence

CC CC consisting of at least three contiguous amino acids of groups R1-R8 in

CC CC the sequence of formula R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together

CC CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,

CC CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane

CC CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoSer or

CC CC azatyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or

CC CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Bt), Ile or Tyr, Ra and Rb are

CC CC not defined in the specification, the peptide bond between Ra and Rb is

CC CC labile to aminopeptidase A cleavage excluding sequences including R4 as a

CC CC terminal Tyr group. A second active agent comprising a sequence

CC CC consisting of at least three contiguous amino acids of groups R2-R8 in

CC CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,

CC CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also

CC CC described. The inventions are particularly useful in cell culture

CC CC mediums. These cells may be used in transplantation techniques for

CC CC treatment of malignant or inherited diseases. The formulae represent

CC CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),

CC CC or AII AT2 type 2 receptor agonists.

XX CC Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

DB 1 drvyi 5

RESULT 3

AAW65605

ID AAW65605 standard; peptide; 5 AA.

XX AC AAW65605;

XX AC AAW65605;

XX 09-NOV-1998 (first entry)

XX DE Angiotensin II analogue, AII(1-5).

XX KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;

XX KW wound healing.

XX OS Synthetic.

OS Homo sapiens.

XX WO9826795-A1.

XX PN 25-JUN-1998.

XX PF 16-DEC-1997; 97WO-US23461.

XX PR 15-DEC-1997; 97US-0990664.

XX PR 16-DEC-1996; 96US-0028310.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega GS, Rodgers KE;

XX DR WPI; 1998-362518/31.

XX PT Promoting incorporation of skin graft onto underlying tissue -

XX PT comprises pre-treating graft with angiotensin II, or analogue or

PT peptide fragment  
PS Disclosure; Page 6; 82pp; English.  
XX  
CC The invention relates to the use of angiotensin II (AII), AII analogues,  
CC AII fragments and AII fragment analogues for promoting incorporation of a  
CC skin graft into underlying tissue of a mammal. The peptides are effective  
CC in accelerating the growth or healing of skin grafts and in accelerating  
CC re-epithelialisation and tissue repair, even at very low concentrations.  
CC They can significantly accelerate the rate of healing at nanomolar levels  
CC in vivo. AII accelerates wound repair by increased neovascularisation,  
CC growth factor release, re-epithelialisation, extracellular matrix production  
CC and increased flow of blood and nutrients to the injured tissue. Use of  
CC the above peptides other than AII itself (an extremely potent vaso-  
CC constrictor) may avoid the side-effects of AII, such as increase in blood  
CC pressure and thirst. The present sequence represents an angiotensin  
CC II fragment.  
XX  
SQ Sequence 5 AA;  
  
Query Match 100.0%; Score 26; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DRVYI 5  
Db 1 drvy1 5  
|||||  
  
RESULT 4  
AAW71118  
ID AAW71118 standard; peptide; 5 AA.  
XX  
AC AAW71118;  
XX  
DT 27-OCT-1998 (first entry)  
XX  
DE Peptide AII(1-5) used to accelerate thermal wound healing.  
XX  
XX Angiotensin; AII; acceleration; thermal wound healing; human;  
KW growth factor release; neovascularisation; re-epithelialisation;  
KW extracellular matrix production.  
XX  
OS Synthetic.  
XX  
PN WO9833813-A2.  
XX  
PD 06-AUG-1998.  
XX  
PF 04-FEB-1998; 98WO-US02049.  
XX  
PR 04-FEB-1997; 97US-0037166.  
XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX  
PI Dizerega G, Rodgers KE;  
XX  
DR WPI; 1998-437391/37.  
XX  
XX Methods for accelerating thermal wound healing in humans - using  
PT angiotensinogen II and AII analogues  
PT  
PS Claim 3; Page 9; 58pp; English.  
XX  
CC AAW71110-27 represent peptide used in the method of the invention. The  
CC specification describes a method of accelerating thermal wound healing  
CC in humans. The method comprises applying to the thermally injured tissue  
CC an amount of at least one active agent which comprises the peptides  
CC AAW71115-27. The method can be used to promote the healing of thermal  
CC wounds by accelerating growth factor release, neovascularisation,  
CC re-epithelialisation and extracellular matrix production. The sequences  
CC are analogues of the angiotensin or angiotensinogen family of proteins.

XX  
SQ Sequence 5 AA;  
  
Query Match 100.0%; Score 26; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DRVYI 5  
Db 1 drvy1 5  
|||||  
  
RESULT 5  
AAAY49594  
ID AAY49594 standard; peptide; 5 AA.  
XX  
AC AAY49594;  
XX  
DT 13-JAN-2000 (first entry)  
XX  
DE Angiotensin analogue peptide SEQ ID NO:9.  
XX  
XX Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;  
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.  
XX  
OS Synthetic.  
XX  
PN WO9952540-A1.  
XX  
PD 21-OCT-1999.  
XX  
PF 07-APR-1999; 99WO-US07654.  
XX  
PR 09-APR-1998; 98US-0081262.  
XX  
PR 12-JUN-1998; 98US-0089024.  
XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX  
PI Rodgers KE, Dizerega G;  
XX  
DR WPI; 1999-620285/53.  
XX  
PT Treating or preventing infections in mammals using peptides derived  
PT from angiotensin or angiotensin receptor agonists  
XX  
PS Claim 2; Page 10; 91pp; English.  
XX  
XX The present invention describes a method for treating or preventing  
CC infections in mammals by administering peptides (A) that are fragments  
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or  
CC II, or angiotensin II AT<sub>2</sub>-type receptor agonists (A) contain at least  
CC 3 consecutive amino acids (aa) from the sequence (S1):  
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;  
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane  
CC carboxylic acid), Ala, dimethylglycine, pro, betaine, Glu(NH<sub>2</sub>), Gly,  
CC Asp(NH<sub>2</sub>) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,  
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,  
CC Ile, Gly, Pro, Alb (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr  
CC (Optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;  
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;  
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =  
CC sequences having R4 as a terminal Tyr residue are excluded. The method  
CC is particularly used in cases of bacterial infection (e.g. septic shock,  
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and  
CC parasitic infections. AAY49586 to AAY49623 represent specifically  
CC claimed examples of (A).  
XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
| | | | |  
Db 1 drvyi 5

## RESULT 6

AAV33909  
ID AAY33909 standard; peptide; 5 AA.

XX AC AAY33909;

XX DT 29-NOV-1999 (first entry)

XX DE Angiotensin II analogue AII(1-5).

XX KW embryonic stem cell; ES; angiotensin; totipotent cell;  
KW gene therapy; replacement therapy; angiotensin II; AII;  
KW analogue.

XX OS Homo sapiens.

XX PN W09942122-A1.

XX PD 26-AUG-1999.

XX PF 16-FEB-1999; 99WO-US03243.

XX PR 19-FEB-1998; 98US-0075179.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX DR WPI; 1999-527419/44.

XX PT Promoting embryonal cell proliferation, using angiotensinogen and  
XX angiotensin peptides, analogs or fragments

XX PS Claim 2; Page 8; 76pp; English.

XX CC This is the amino acid sequence of the Angiotensin II analogue,  
CC AII(1-5). The formation of Angiotensin II (AII) is initiated by the  
CC action of renin on the plasma substrate angiotensinogen.

CC CC This results in Angiotensin I (AI) which then converted to AII by the  
CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
CC residues from AI (AAY42372).

CC CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and  
CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,  
CC or AII AT2 type 2 receptor agonists can rapidly provide a large

CC CC population of ESCs (Embryonic Stem Cell) for use in replacement  
CC therapy. Similarly, methods that increase in vivo proliferation of  
CC ESCs will enhance the utility of replacement therapy by rapidly

CC CC increasing local concentration of the stem cells and their progeny at  
CC the site of therapy.

CC CC The method also increases the potential utility of ESCs as vehicles  
CC for gene therapy in certain disorders by more efficiently providing  
CC a large number of such cells for transfection, and also by providing a

CC CC more efficient means to rapidly expand transduced ESCs.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
| | | | |  
Db 1 drvyi 5

## RESULT 7

AAV30547

ID AAY30547 standard; peptide; 5 AA.

XX AC AAY30547;

XX DT 18-NOV-1999 (first entry)

XX DE Amino acid sequence of angiotensin II fragment AII1-5.

XX KW Angiotensin; analogue; tissue equivalent; cell proliferation.

XX OS Synthetic.

XX PN W09946285-A2.

XX PD 16-SEP-1999.

XX PF 11-MAR-1999; 99WO-US05261.

XX PR 11-MAR-1998; 98US-0077499.

XX PR 12-JUN-1998; 98US-0089064.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers KE, Dizerega G;

XX DR WPI; 1999-551360/46.

XX PT An improved method for producing a tissue equivalent with angiotensin I

XX PT and II derived active agents -

XX PS Claim 2; Page 56; 83pp; English.

XX CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII  
XX fragments and AII analogues. The peptides are used in the method  
XX of the invention. The specification describes an improved method  
XX for producing a tissue equivalent. The method comprises contacting  
XX the tissue equivalent with angiotensin I and II derived active  
XX agents. The methods are used for production and culture of tissue  
XX equivalents (three-dimensional cell and tissue culture systems),  
XX chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,  
XX vascular graft, cartilage, ligament, collagen lattice, liver and  
XX kidney tissue equivalents. The methods and tissue culture systems  
XX are used for the long-term proliferation of cells and tissues  
XX in an in vitro environment that more closely approximates that found  
XX in vivo.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

| | | | |

Db 1 drvyi 5

## RESULT 8

AAV30591

ID AAY30591 standard; peptide; 5 AA.

XX AC AAY30591;

XX DT 18-NOV-1999 (first entry)

XX DE Amino acid sequence of an angiotensin II (AII) fragment AII1-5.

XX KW Angiotensin; analogue; radiation mitigation; tissue damage;

XX KW radiation therapy; bone marrow transplantation;

XX KW megakaryocyte production; platelet production; cancer therapy;

KW gene therapy; hematopoietic disorder.

OS Synthetic.

PN WO9945945-A1.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US05194.

XX 10-MAR-1998; 98US-0077382.

PR 09-APR-1998; 98US-0081262.

PR 30-APR-1998; 98US-0083670.

PR 19-JUN-1998; 98US-0090096.

PR 22-JUN-1998; 98US-0090216.

PR 11-SEP-1998; 98US-0099957.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

PA (RODG/) RODGERS K E.

PA (DIZE/) DIZEREGA G.

XX Rodgers KE, Dizerega G;

PI WPI; 1999-551209/46.

DR Use of angiotensin and angiotensin type peptides, for mitigating

PT radiation induced tissue damage, improving bone marrow transplantation

PT and promoting megakaryocyte and platelet production

XX Claim 2; Page 89; 116pp; English.

XX AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII

CC fragments and AII analogues. The peptides are used in the method

CC of the invention. The specification describes a method for mitigating

CC radiation induced tissue damage, improving the effectiveness of

CC radiation therapy, to support bone marrow transplantation, and

CC promoting megakaryocyte production and mobilization and platelet

CC production. The method comprises administration of the present peptides.

CC The methods can be used to mitigate radiation induced tissue damage, to

CC improve the effectiveness of radiation therapy, to support bone marrow

CC transplantation, and to promote megakaryocyte production and

CC mobilization and platelet production. They are used particularly in

CC cancer therapy. They can also be used to provide megakaryocytes as

CC vehicles for gene therapy in hematopoietic disorders, by providing a

CC more efficient means to rapidly expand transduced megakaryocytes.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5

Db 1 drvyi 5

RESULT 9

AAY32722

ID AAY32722 standard; peptide; 5 AA.

XX AAY32722;

AC AAY32722;

XX 09-NOV-1999 (first entry)

DT Angiotensin II analogue AII(1-5).

DE Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;

XX chemotaxis; growth factor; liver regeneration; cirrhosis;

KW hepatocarcinoma; hepatectomy; transplantation.

XX Synthetic.

OS Homo sapiens.

PN WO9939743-A2.

XX 12-AUG-1999.

XX 08-FEB-1999; 99WO-US02618.

XX 13-NOV-1998; 98US-0108412.

PR 09-FEB-1998; 98US-0074104.

XX (DIZE/) DIZEREGA G.

PA (RODG/) RODGERS K E.

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

PI WPI; 1999-508461/42.

XX Hepatic cell proliferation with angiotensin I and II derived active

DR agents, useful for regeneration of liver after resection

PA Claim 2; Page 9; 66pp; English.

PT Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The

PI peptides are derived from the AII peptide (AAY32750). AII increases

DR mitogenesis and chemotaxis in cultured cells, and also increases the

DR release of growth factors and extracellular matrices. AII has also been

XX shown to increase the proliferation of certain cell types. The AII

XX analogue peptides can be used as the active agent in a method for

XX promoting hepatic cell proliferation and differentiation. The method

XX involves contacting the hepatic cells with an amount effective enough to

XX promote proliferation of any of the peptides. This method is useful in

XX liver regeneration following resection of hepatocarcinomas, hepatitis

XX infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic

XX failure, hepatocyte transplantation, liver transplantation and other

XX hepatic disorders where rapid regeneration of the liver is desirable. The

XX methods are also useful in rapidly providing a large population of

XX hepatic cells for use in cell therapy and for providing a large

XX population of transduced hepatic cells for use in gene therapy.

XX Sequence 5 AA;

SQ Query Match 100.0%; Score 26; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5

Db 1 drvyi 5

RESULT 10

AAY33776

ID AAY33776 standard; peptide; 5 AA.

XX AAY33776;

AC AAY33776;

XX 09-NOV-1999 (first entry)

DT Angiotensin II (AII) octapeptide fragment AII(1-5).

DE Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;

XX neuronal cell proliferation; differentiation; Alzheimer's disease;

KW Parkinson's disease; neuron replacement therapy.

XX Homo sapiens.

OS WO9942123-A1.

PN 26-AUG-1999.

XX

PF 19-FEB-1999; 99WO-US03772.

XX PS  
XX PR 19-FEB-1998; 98US-0075232.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX XX WPI; 1999-527420/44.

XX XX Promoting neuronal cell proliferation and differentiation

XX PT Claim 2; Page 10; 62pp; English.

XX PS Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin  
XX CC II (AII) octapeptide (AAY33768) and they have AII agonist activity. The  
XX CC application of angiotensin to wound tissue significantly increases the  
XX CC rate of wound healing. AII is known to increase mitogenesis and  
XX CC chemotaxis in cultured cells, and also increases their release of growth  
XX CC factors and extracellular matrices, implicating it in cell growth and  
XX CC differentiation. AT2 receptors are receptors for AII and are thought to  
XX CC be involved in the mediation of the cell differentiation effects of AII.  
XX CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal  
XX CC cell proliferation or differentiation. This method is useful in the  
XX CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement  
XX CC therapy.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

DB 1 DRVYI 5

RESULT 11

AAV15353

ID AAY15353 standard; peptide; 5 AA.

XX AC AAY15353;

XX DT 09-NOV-1999 (first entry)

XX DE Angiotensin II (AII) analogue, AII(1-5).

XX KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;  
XX KW AII; analogue; chronic renal failure; cancer; bone marrow.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9940106-A2.

XX PD 12-AUG-1999.

XX PF 08-FEB-1999; 99WO-US02648.

XX PR 09-DEC-1998; 98US-0111535.

XX PR 09-FEB-1998; 98US-0074106.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX XX WPI; 1999-508486/42.

XX XX Promoting erythropoiesis with angiotensin I and II derived active  
XX PT agents, useful for treatment of, e.g. congenital or acquired  
XX PT aplastic or hypoplastic anemia

XX

PS Claim 2; Page 10; 76pp; English.

XX CC This sequence is an angiotensin II (AII) analogue. Similar sequences  
XX CC also based on the AII peptide have been tested against each other, AII  
XX CC and a negative control. These active agents have been shown to affect  
XX CC the levels of BFU-E (burst forming units-erythroid) in culture.  
XX CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)  
XX CC augment erythropoiesis by potentiating erythropoietin-induced  
XX CC differentiation. Increasing the rate of erythropoiesis improves clinical  
XX CC benefits for the treatment of congenital or acquired aplastic or  
XX CC hypoplastic anemia associated with chronic renal failure, end-stage renal  
XX CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,  
XX CC bone marrow transplantation and chronic diseases.

XX CC The active agents permit the use of smaller doses of erythropoietin  
XX CC therefore decreasing treatment costs.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

DB 1 DRVYI 5

RESULT 12

AAV15313

ID AAY15313 standard; peptide; 5 AA.

XX AC AAY15313;

XX DT 09-NOV-1999 (first entry)

XX DE Angiotensin II (AII) analogue, AII(1-5).

XX KW angiotensin; angiotensin II; AII; wound healing; scarring;

XX KW tissue repair; agonist; analogue.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9940107-A2.

XX PD 12-AUG-1999.

XX PF 08-FEB-1999; 99WO-US02725.

XX PR 09-FEB-1998; 98US-0074105.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX XX WPI; 1999-508487/42.

XX XX Epithelial stem cell and keratinocyte proliferation with angiotensin  
XX PT I and II derived active agents, useful for treatment of skin wounds

XX PS Claim 2; Page 10; 70pp; English.

XX CC This is the amino acid sequence of an Angiotensin II analogue. This and  
XX CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)  
XX CC can be used to promote the proliferation of epithelial stem cells and  
XX CC keratinocytes leading to a more rapid and efficient cellular response to  
XX CC stratified epithelial injury. The angiotensin analogues are derived from  
XX CC an octapeptide present in humans and other species which has the  
XX CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as  
XX CC angiotensin II (AII). This is formed by the action of renin on the  
XX CC plasma substrate angiotensinogen, the product of this reaction is a



CC decapeptide called angiotensin I (AI) which is converted to AII by the  
 CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
 CC residues from AI (AA15339).  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 |||||  
 Db 1 drvyi 5

RESULT 13  
 AAB27409  
 ID AAB27409 standard; Peptide; 5 AA.

XX AAB27409;  
 XX  
 DT 23-JAN-2001 (first entry)  
 XX  
 DE Angiotensin II analog AII(1-5).

XX Angiotensinogen; AII: AII: myocyte proliferation; myocardial injury;  
 KW cardiomyopathies; inflammation; infection; sepsis; ischemia;  
 KW heart valve disease; myocarditis; angiotensin.

XX Synthetic.

XX WO200053211-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US06198.

XX 09-MAR-1999; 99US-0123678.

XX 31-AUG-1999; 99US-0151874.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers K, Dizerega G;

XX WPI; 2000-611400/58.

XX Promoting myocyte proliferation and myocardial tissue repair by  
 PT contacting myocytes with angiotensinogen or angiotensin I or II, useful  
 PT for treating heart attacks, cardiomyopathies, inflammation and  
 PT infection.

PS Claim 2; Page 10; 55pp; English.

XX The present invention relates to a method of promoting myocyte  
 CC proliferation or differentiation by contacting myocytes with an active  
 CC agent containing angiotensinogen, angiotensin I and II (AI, AII), and  
 CC angiotensin analogs. The present sequence is an angiotensin II analog  
 CC of the invention. The active agents of the invention may be useful for  
 CC promoting myocardial tissue repair following myocardial injury and for  
 CC treating heart failure in a mammal. Administration to accelerate in  
 CC vivo myocyte proliferation and/or to treat myocardial injuries can be  
 CC used to treat cardiomyopathies, inflammation, infection, sepsis,  
 CC ischemia, heart valve disease, myocarditis, inflammation, myocardial  
 CC ischemia and infarction and for improving cardiac output by increasing  
 CC stroke volume.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 |||||  
 Db 1 drvyi 5

RESULT 14  
 AAB28107  
 ID AAB28107 standard; Peptide; 5 AA.

XX AAB28107;

XX 26-JAN-2001 (first entry)

XX Angiotensin II analogue SEQ ID NO: 9.

XX Wound; scar formation; healing; adhesion formation; AII;  
 KW angiotensin II analogue; scar treatment.

XX Synthetic.

XX WO200056345-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-US07669.

XX 23-MAR-1999; 99US-0125707.

XX 16-JUN-1999; 99US-0139541.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers K, Dizerega G;

XX WPI; 2000-587607/55.

XX Limiting scar or adhesion formation comprises administering at least  
 PT one active agent comprising a peptide.

PS Claim 2; Page 10; 54pp; English.

XX The present invention is concerned with peptide analogues of angiotensin  
 CC II (AII) which can be used to limit scar and adhesion formation. The  
 CC application of AII to wound tissue results in a rapid increase in the  
 CC rate of wound healing and causes the proliferation of certain cells, such  
 CC as epithelial cells and keratinocytes. Analogues of the protein have been  
 CC shown to reduce scar formation, and can be used not only to limit new  
 CC scar formation but also to therapeutically treat existing scars. The  
 CC wound types include lacerations, burns, punctures, trauma, ulcers,  
 CC periodontal conditions, laparotomy and incisional wounds, revision of  
 CC hypertrophic scars, genetic hypertrophic scars, keloid scars,  
 CC contractures after burns and cosmetic surgical procedures.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 |||||  
 Db 1 drvyi 5

RESULT 15  
 AAY84568  
 ID AAY84568 standard; Peptide; 5 AA.

XX AAY84568;

XX 25-JUL-2000 (first entry)

DE Amino acid sequence of angiotensin I conversion product Ang(1-5).  
XX  
KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);  
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;  
KW chronic heart failure; acute heart failure; myocardial infarction;  
KW renal failure.  
XX  
XX Homo sapiens.  
OS  
XX WO200018899-A2.  
PN  
XX  
XX PD 06-APR-2000.  
XX  
XX 29-SEP-1999; 99WO-US22976.  
XX  
XX 30-SEP-1998; 98US-0163648.  
PR  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX  
XX Acton LS, Robison KE, Hsieh FY;  
PI  
XX WPI; 2000-293140/25.  
DR  
XX  
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)  
PT polypeptide useful for detecting an ACE-2 therapeutic for treating  
PT hypertension, congestive heart failure, myocardial infarction,  
PT atherosclerosis and renal failure -  
XX  
XX Disclosure; Fig 8; 138pp; English.  
PS  
XX  
XX AAY84563-68 represent angiotensin I conversion products. The  
CC specification describes a human angiotensin converting enzyme-2 (ACE-2).  
CC ACE-2 is expressed predominantly in kidneys and testis. The sequence of  
CC the full length ACE-2 cDNA was determined from a clone obtained from a  
CC cDNA library prepared from mRNA of a human heart of a subject who had  
CC congestive heart failure. ACE-2 has significant sequence homologies with  
CC ACE enzymes, and has also been shown to hydrolyse angiotensin I into  
CC Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure  
CC related diseases and conditions, such as hypertension, congestive heart  
CC failure, chronic heart failure, acute heart failure, myocardial  
CC infarction, atherosclerosis and renal failure.  
XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
| | | | |  
Db 1 drvyi 5

Search completed: July 1, 2002, 07:41:55  
Job time: 347 sec

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Run On: July 1, 2002, 07:43:01 ; Search time 59.1 Seconds  
(without alignments)  
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Title: US-09-723-197-9  
Perfect score: 26  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	26	100.0	5	3	US-09-208-337-9
3	26	100.0	5	3	US-08-990-664-10
4	26	100.0	5	4	US-09-373-962-9
5	26	100.0	5	4	US-09-245-680-9
6	26	100.0	5	4	US-09-198-806C-9
7	26	100.0	5	4	US-09-352-191-9
8	26	100.0	5	4	US-09-012-400-9
9	26	100.0	6	2	US-08-465-775-8
10	26	100.0	6	3	US-09-208-337-8
11	26	100.0	6	3	US-08-990-664-9
12	26	100.0	6	4	US-09-373-962-8
13	26	100.0	6	4	US-09-245-680-8
14	26	100.0	6	4	US-09-198-806C-8
15	26	100.0	6	4	US-09-352-191-8
16	26	100.0	6	4	US-09-012-400-8
17	26	100.0	7	2	US-08-465-775-4
18	26	100.0	7	3	US-09-208-337-4
19	26	100.0	7	3	US-08-990-664-5
20	26	100.0	7	4	US-09-373-962-4
21	26	100.0	7	4	US-09-245-680-4
22	26	100.0	7	4	US-09-198-806C-4
23	26	100.0	7	4	US-09-352-191-4
24	26	100.0	7	4	US-09-012-400-4
25	26	100.0	7	6	5451571-4
26	26	100.0	8	1	US-07-858-842-2
27	26	100.0	8	1	US-08-021-839A-3

28	26	100.0	8	1	US-08-184-935-2	Sequence 2, Appli
29	26	100.0	8	1	US-08-212-433A-29	Sequence 29, Appli
30	26	100.0	8	1	US-08-185-448-8	Sequence 8, Appli
31	26	100.0	8	1	US-07-776-272-1	Sequence 1, Appli
32	26	100.0	8	1	US-08-428-488-21	Sequence 21, Appli
33	26	100.0	8	1	US-08-337-781-1	Sequence 1, Appli
34	26	100.0	8	1	US-08-240-711-20	Sequence 20, Appli
35	26	100.0	8	1	US-08-594-117-1	Sequence 1, Appli
36	26	100.0	8	1	US-08-520-770-2	Sequence 2, Appli
37	26	100.0	8	1	US-08-457-753-20	Sequence 20, Appli
38	26	100.0	8	2	US-08-115-968-1	Sequence 1, Appli
39	26	100.0	8	2	US-08-115-968-3	Sequence 3, Appli
40	26	100.0	8	2	US-08-115-968-4	Sequence 4, Appli
41	26	100.0	8	2	US-08-465-774-1	Sequence 1, Appli
42	26	100.0	8	2	US-08-465-774-2	Sequence 2, Appli
43	26	100.0	8	2	US-08-360-784B-2	Sequence 2, Appli
44	26	100.0	8	2	US-08-623-833B-4	Sequence 4, Appli
45	26	100.0	8	2	US-08-465-775-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-465-775-9  
; Sequence 9, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: digerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-775-9

Query Match 100.0%; Score 26; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYI 5  
Db 1 DRVYI 5

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RESULT 2
US-09-208-337-9
; Sequence 9, Application US/09208337
; Patent No. 6096709
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gere, dizerega
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,337
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,775
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/337,781
; FILING DATE: 14-NOV-1994
; APPLICATION NUMBER: 08/126,368
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC010.001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 949-760-0404
; TELEFAX: 949-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-208-337-9

Query Match 100.0%; Score 26; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 3
US-08-990-664-10
; Sequence 10, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; TITLE OF INVENTION: IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
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; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,664
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,310
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC012.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-990-664-10

Query Match 100.0%; Score 26; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 4
US-09-373-962-9
; Sequence 9, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
; FILE REFERENCE: 98364A
; CURRENT APPLICATION NUMBER: US/09/373,962
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-373-962-9

Query Match 100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5
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RESULT 5  
US-09-245-680-9  
; Sequence 9, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245,680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-245-680-9

Query Match 100.0%; Score 26; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|  
|  
|  
|  
Db 1 DRVYI 5

RESULT 6  
US-09-198-806C-9  
; Sequence 9, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-198-806C-9

Query Match 100.0%; Score 26; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|  
|  
|  
|  
Db 1 DRVYI 5

RESULT 7  
US-09-352-191-9  
; Sequence 9, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue

; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352,191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-352-191-9

Query Match 100.0%; Score 26; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|  
|  
|  
|  
Db 1 DRVYI 5

RESULT 8  
US-09-012-400-9  
; Sequence 9, Application US/09012400D  
; Patent No. 6335195  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell  
; TITLE OF INVENTION: Proliferation and Differentiation  
; FILE REFERENCE: 97,017-G  
; CURRENT APPLICATION NUMBER: US/09/012,400D  
; CURRENT FILING DATE: 1998-01-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-012-400-9

Query Match 100.0%; Score 26; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|  
|  
|  
|  
Db 1 DRVYI 5

RESULT 9  
US-08-465-775-8  
; Sequence 8, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,775  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-360  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 8:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-775-8

Query Match 100.0%; Score 26; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 1 DRVYI 5

RESULT 10  
US-09-208-337-8  
Sequence 8, Application US/09208337  
Patent No. 6096709  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: Gere, dizegga  
TITLE OF INVENTION: USE OF ANGIOGENSIN II FRAGMENTS  
TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/208,337  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,775  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: 08/337,781  
FILING DATE: 14-NOV-1994  
APPLICATION NUMBER: 08/126,368  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: USC010.001CP2  
TELEPHONE: 949-760-0404

TELEFAX: 949-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-208-337-8

Query Match 100.0%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 1 DRVYI 5

RESULT 11  
US-08-990-664-9  
Sequence 9, Application US/08990664  
Patent No. 6110895  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: dizegga, Gere  
TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
TITLE OF INVENTION: IN SKIN GRAFTS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/990,664  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,310  
FILING DATE: 16-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: USC012.001A  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-990-664-9

Query Match 100.0%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 1 DRVYI 5  
|||||

## RESULT 12

US-09-373-962-8  
; Sequence 8, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-373-962-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
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Db 1 DRVYI 5

## RESULT 13

US-09-245-680-8  
; Sequence 8, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245,680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-245-680-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
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Db 1 DRVYI 5

## RESULT 14

US-09-198-806C-8  
; Sequence 8, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-198-806C-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||

Db 1 DRVYI 5

## RESULT 15

US-09-352-191-8  
; Sequence 8, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue  
; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352,191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-352-191-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||

Db 1 DRVYI 5

Search completed: July 1, 2002, 07:43:01  
Job time: 302 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:29 ; Search time 69.93 Seconds  
(without alignments)  
6.870 Million cell updates/sec

Title: US-09-723-197-9  
Perfect score: 26  
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	26	100.0	14	2	A01250	angiotensin precu
3	26	100.0	15	2	A60834	angiotensin I prec
4	26	100.0	115	2	A48793	glycosylation-inhi
5	26	100.0	115	2	I52370	macrophage migrati
6	26	100.0	115	2	A44499	macrophage migrati
7	26	100.0	115	2	C47274	migration inhibito
8	26	100.0	167	2	F83685	hypothetical prote
9	26	100.0	195	1	B69441	conserved hypothet
10	26	100.0	238	2	E70337	ABC transporter -
11	26	100.0	248	2	T44932	3-oxoacyl-l-acyl-ca
12	26	100.0	312	2	T00992	hypothetical prote
13	26	100.0	314	2	G73799	phoE protein U5922
14	26	100.0	328	2	AF2597	hypothetical prote
15	26	100.0	396	2	AD0310	hypothetical prote
16	26	100.0	409	1	G69000	molybdenum cofacto
17	26	100.0	476	1	JC2318	angiotensin precu
18	26	100.0	477	1	ANRT	angiotensin precu
19	26	100.0	477	1	A29978	angiotensin precu
20	26	100.0	485	1	ANHU	angiotensin precu
21	26	100.0	509	2	T06300	hypothetical prote
22	26	100.0	518	2	B64449	2-isopropylmalate
23	26	100.0	540	2	S72233	transcription fact
24	26	100.0	575	1	HNNZSZ	hemagglutinin-neu
25	26	100.0	575	1	HNNZSH	hemagglutinin-neu
26	26	100.0	575	2	S12135	hemagglutinin-neu
27	26	100.0	576	1	HNNZS	hemagglutinin-neu
28	26	100.0	581	1	A37913	serine/threonine-s
29	26	100.0	584	2	A97171	uncharacterized pr

30	26	100.0	614	2	T43121	hypothetical prote
31	26	100.0	644	2	G64938	hypothetical prote
32	26	100.0	644	2	F82145	conserved hypothet
33	26	100.0	644	2	D90940	hypothetical prote
34	26	100.0	644	2	H85788	hypothetical prote
35	26	100.0	644	2	AF0262	conserved hypothet
36	26	100.0	644	2	AD0712	conserved hypothet
37	26	100.0	661	2	C83843	hypothetical prote
38	26	100.0	676	1	WMBEX6	UL6 protein - huma
39	26	100.0	688	2	A44306	polyposphate kina
40	26	100.0	688	2	C91049	polyposphate kina
41	26	100.0	688	2	G85893	polyposphate kina
42	26	100.0	688	2	AC0819	polyposphate kina
43	26	100.0	739	2	I40715	malate synthase (E
44	26	100.0	749	2	S77175	sensory transducti
45	26	100.0	778	2	T44761	probable preprotei

ALIGNMENTS

RESULT 1

S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432  
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen  
Eur. J. Biochem. 237, 414-423, 1996  
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte  
A:Reference number: S65431; MUID:96215437  
A:Accession: S65432  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <WIJ>  
A>Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 26; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.4; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 DRVYI 5

Db 1 DRVYI 5

RESULT 2

A01250  
angiotensin precursor - horse (fragment)  
C:Species: Equus caballus (domestic horse)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998  
C:Accession: A92775; A01250  
R:Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957  
A:Reference number: A92775  
A:Accession: A92775  
A:Molecule type: protein  
A:Residues: 1-14 <SKE>

C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 26; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.9;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 1 DRVYI 5

```
RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N:Alternate names: angiotensinogen I
N:Contains: angiotensin I
C:Species: Canis lupus familiaris (dog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C:Accession: A60834
R:Oliver, J.A.
Hypertension 11, 21-27, 1988
A>Title: Purification and partial characterization of canine angiotensinogen.
A:Reference number: A60834; MUID:88113996
A:Accession: A60834
A:Molecule type: protein
A:Residues: 1-15 <OLI>
C:Superfamily: antithrombin III
C:Keywords: glycoprotein; plasma
F:1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
Db 1 DRVYI 5

RESULT 4
A48793
glycosylation-inhibiting factor - human
N:Alternate names: macrophage migration inhibitory 12.7K protein; sarcolectin
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
C:Accession: A48793; A49612; A33838; A47274; S34300; S33277
R:Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993
A>Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-in
A:Reference number: A48793; MUID:94052102
A:Accession: A48793
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-115 <MIK>
A:Cross-references: GB:L10612; NID:g402701; PIDN:AAA35892.1; PID:g402702
R:Paralkar, V.; Wistow, G.
Genomics 19, 48-51, 1994
A>Title: Cloning the human gene for macrophage migration inhibitory factor (MIF).
A:Reference number: A49612; MUID:94245178
A:Accession: A49612
A:Molecule type: DNA
A:Residues: 1-115 <PAR>
A:Cross-references: GB:L19686; NID:g307284; PIDN:AAA21814.1; PID:g307285
R:Weiser, W.Y.; Temple, P.A.; Wittek-Giannotti, J.S.; Remold, H.G.; Clark, S.C.; David, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 7522-7526, 1989
A>Title: Molecular cloning of a cDNA encoding a human macrophage migration inhibitory fa
A:Reference number: A33838; MUID:90017510
A:Accession: A33838
A:Molecule type: mRNA
A:Residues: 1-105,'S',107-115 <WEI>
A:Cross-references: GB:M25639; NID:g188555; PIDN:AAA36315.1; PID:g188556
R:Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A>Title: A macrophage migration inhibitory factor is expressed in the differentiating ce
A:Reference number: A47274; MUID:93165679
A:Accession: A47274
A:Molecule type: mRNA
A:Residues: 10-115 <WIS>
A:Cross-references: GB:M95775; NID:g187180; PIDN:AAA36179.1; PID:g187181
A:Experimental source: fetal lens
A>Note: sequence extracted from NCBI backbone (NCBIN:124868, NCBIPI:124871)
```

```
R:Bucala, R.; Mitchell, R.A.; Bernhagen, J.
submitted to the EMBL Data Library, June 1993
A:Reference number: S34300
A:Accession: S34300
A:Molecule type: mRNA
A:Residues: 1-115 <BUC>
A:Cross-references: EMBL:Z23063; NID:g312333; PIDN:CAA80598.1; PID:g312334
R:Zeng, F.Y.; Weiser, W.Y.; Kratzin, H.; Stahl, B.; Karas, M.; Gabius, H.J.
Arch. Biochem. Biophys. 303, 74-80, 1993
A>Title: The major binding protein of the interferon antagonist sarcolectin in human
A:Reference number: S33277; MUID:93256574
A:Accession: S33277
A:Molecule type: protein
A:Residues: 3-24 <ZEN>
A:Experimental source: placenta
A>Note: there is no signal sequence; the mature protein starts with residue 3
C:Genetics:
A:Gene: GDB:MIF
A:Cross-references: GDB:I38402; OMIM:I53620
A:Map position: 22q11.2-22q11.2
A:Introns: 36/3; 94/2
A>Note: appears to be a single copy gene (see reference A49612)
C:Superfamily: bovine glycosylation-inhibiting factor
F:3-115/Product: macrophage migration inhibitory factor #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
Db 93 DRVYI 97

RESULT 5
I52370
macrophage migration inhibitory factor MIF [similarity] - rat
C:Species: Rattus sp. (rat)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I52370
R:Sakai, M.; Nishihira, J.; Hibiya, Y.; Koyama, Y.; Nishi, S.
Biochem. Mol. Biol. Int. 33, 439-446, 1994
A>Title: Glutathione binding rat liver 13k protein is the homologue of the macrophage
A:Reference number: I52370; MUID:95038523
A:Accession: I52370
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-115 <RES>
A:Cross-references: GB:S73424; NID:g663139; PIDN:AAB32392.1; PID:g663140
C:Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
Db 93 DRVYI 97

RESULT 6
A44499
macrophage migration inhibitory factor DER6 - mouse
N:Alternate names: glycosylation-inhibiting factor; migration inhibitory factor, 10K
C:Species: Mus musculus (house mouse)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A44499; S34299; B47274; I49691; S38325; I56259
R:Lanahan, A.; Williams, J.B.; Sanders, L.K.; Nathans, D.
Mol. Cell. Biol. 12, 3919-3929, 1992
A>Title: Growth factor-induced delayed early response genes.
A:Reference number: A44499; MUID:92375060
```

A:Accession: A44499  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-115 <LAN>  
A:Experimental source: BALB/c 3T3 cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:111643)  
R:Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.; Tracey, K.J.; Manogue, K.; Vogt  
submitted to the EMBL Data Library, June 1993  
A:Reference number: S34299  
A:Accession: S34299  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-115 <BER>  
A:Cross-references: EMBL:223048; NID:g312220; PIDN:CAA80583.1; PID:g312221  
R:Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993  
A:Title: A macrophage migration inhibitory factor is expressed in the differentiating ce  
A:Reference number: A47274; MUID:93163679  
A:Accession: B47274  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 6-115 <WIS>  
A:Cross-references: GB:L07607; NID:g191490; PIDN:AAA37111.1; PID:g191491  
A:Experimental source: lens  
A:Note: sequence extracted from NCBI backbone (NCBIN:124869, NCBIP:124872)  
R:Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993  
A:Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-in  
A:Reference number: A48793; MUID:94052102  
A:Accession: 149691  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <RES>  
A:Cross-references: GB:L10613; NID:g402716; PIDN:AAA37693.1; PID:g402717  
R:Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.B.; Tracey, K.J.; Voelter, W.;  
Nature 365, 756-759, 1993  
A:Title: MIF is a pituitary-derived cytokine that potentiates lethal endotoxaemia.  
A:Reference number: S38325; MUID:94019845  
A:Accession: S38325  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 2-28 <BE2>  
A:Cross-references: EMBL:223048  
R:Mitchell, R.; Bacher, M.; Bernhagen, J.; Pushkarskaya, T.; Seldin, M.F.; Bucala, R.  
J. Immunol. 154, 3863-3870, 1995  
A:Title: Cloning and characterization of the gene for mouse macrophage migration inhibi  
A:Reference number: 156259; MUID:95221891  
A:Accession: 156259  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-115 <RE2>  
A:Cross-references: GB:L39357; NID:g790847; PIDN:AAA74321.1; PID:g790848  
C:Genetics:  
A:Gene: Mif  
A:Introns: 36/3; 94/2  
C:Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 93 DRVYI 97

RESULT 7  
C47274  
migration inhibitory factor, 10K - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C:Accession: C47274

R:Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993  
A:Title: A macrophage migration inhibitory factor is expressed in the differentiating  
A:Reference number: A47274; MUID:93163679  
A:Accession: C47274  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-115 <WIS>  
A:Cross-references: GB:M95776; NID:g212257; PIDN:AAA48939.1; PID:g212258  
A:Experimental source: embryo, lens  
A:Note: sequence extracted from NCBI backbone (NCBIN:124870, NCBIP:124873)  
C:Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 93 DRVYI 97

RESULT 8  
F83686  
hypothetical protein BH0294 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: F83686  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: F83686  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-167 <STO>  
A:Cross-references: GB:AP001508; GB:BA000004; NID:gi0172890; PIDN:BA04013.1; GSPDB:G  
C:Genetics:  
A:Gene: BH0294

Query Match 100.0%; Score 26; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 61 DRVYI 65

RESULT 9  
B69441  
conserved hypothetical protein AF1531 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: B69441  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes,  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch  
A:Reference number: A69250; MUID:98049343  
A:Accession: B69441  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-195 <KLE>  
A:Cross-references: GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB89717.1; PID:g264  
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0038

Query Match 100.0%; Score 26; DB 1; Length 195;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||  
DB 68 DRVYI 72

RESULT 10  
E70337  
ABC transporter - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 02-Feb-2001  
C:Accession: E70337  
C:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666  
A:Accession: E70337  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-238 <AQF>  
A:Cross-references: GB:AE000689; NID:g2983082; PIDN:AAC06695.1; PID:g2983089; GB:AE00065  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: abcT7  
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology  
C:Keywords: ATP; nucleotide binding; P-loop  
F:17-210/Domain: ATP-binding cassette homology <ABC>  
F:34-41/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 26; DB 2; Length 238;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||  
DB 202 DRVYI 206

RESULT 11  
T44932  
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - Agrobacterium tum  
C:Species: Agrobacterium tumefaciens  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T44932  
R:Kim, K.S.; Farrand, S.K.  
J. Bacteriol. 178, 3275-3284, 1996  
A:Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine man  
by the plant tumor.  
A:Reference number: 222872; MUID:96236046  
A:Accession: T44932  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-248 <KIM>  
A:Cross-references: EMBL:U19620; NID:g797330; PIDN:AAB07783.1; PID:g797334  
A:Experimental source: strain 15955  
C:Genetics:  
A:Gene: mocC  
A:Genome: plasmid pTil5955  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C:Keywords: oxidoreductase

Query Match 100.0%; Score 26; DB 2; Length 248;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 221 DRVYI 225  
|||||

RESULT 12  
T00992  
hypothetical protein At2g26590 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein T9J22.26  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 23-Mar-2001  
C:Accession: T00992; D84662  
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K  
submitted to the EMBL Data Library, April 1998  
A:Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.  
A:Reference number: Z14161  
A:Accession: T00992  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-312 <ROU>  
A:Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739383  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: D84662  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-312 <STO>  
A:Cross-references: GB:AE002093; NID:g2739383; PIDN:AAC14506.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g26590; T9J22.26  
A:Map position: 2  
A:Introns: 11/3; 42/3; 62/3; 100/3; 124/2; 169/2; 210/1; 241/3; 267/3; 286/1

Query Match 100.0%; Score 26; DB 2; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||  
DB 81 DRVYI 85

RESULT 13  
G97379  
phoE protein U59229 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C:Accession: G97379  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldm  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium  
A:Reference number: A97359; PMID:11743194  
A:Accession: G97379  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-314 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK85992.1; PID:g15155055; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_285  
A:Map position: circular chromosome

Query Match 100.0%; Score 26; DB 2; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 94 DRVYI 98  
|||||

## RESULT 14

AF2597  
hypothetical protein phnE [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
C:Accession: AF2597  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; PMID:11743193  
A:Accession: AF2597  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-328 <KUR>  
A:Cross-references: GB:AE008688; PIDN:AAL41196.1; PID:gl7738497; GSPDB:GN00186  
C:Genetics:  
A:Gene: phnE  
A:Map position: circular chromosome

Query Match 100.0%; Score 26; DB 2; Length 328;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 108 DRVYI 112

## RESULT 15

AD0310  
hypothetical protein YPO2542 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AD0310  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001.  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AD0310  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-396 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC91344.1; PID:gl5980533; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO2542

Query Match 100.0%; Score 26; DB 2; Length 396;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 19 DRVYI 23

Search completed: July 1, 2002, 07:46:30  
Job time: 451 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:09 ; Search time 34.05 Seconds  
(without alignments)  
5.686 Million cell updates/sec

Title: US-09-723-197-9  
Perfect score: 26  
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	26	100.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
2	26	100.0	14	1 ANGT_HORSE	P01016 equus cabal
3	26	100.0	114	1 MIF_CHICK	Q02960 gallus gall
4	26	100.0	114	1 MIF_HUMAN	P14174 homo sapien
5	26	100.0	114	1 MIF_MOUSE	P34884 mus musculu
6	26	100.0	114	1 MIF_RAT	P30904 rattus norv
7	26	100.0	436	1 TBX6_HUMAN	O95947 homo sapien
8	26	100.0	476	1 ANGT_SHEEP	P20757 ovis aries
9	26	100.0	477	1 ANGT_MOUSE	P11859 mus musculu
10	26	100.0	477	1 ANGT_RAT	P01015 rattus norv
11	26	100.0	485	1 ANGT_HUMAN	P01019 homo sapien
12	26	100.0	518	1 YB95_METJA	Q58595 methanococc
13	26	100.0	540	1 TBX6_MOUSE	P70327 mus musculu
14	26	100.0	575	1 HEMA_SENDS	P27562 sendai viru
15	26	100.0	575	1 HEMA_SENDF	P19758 sendai viru
16	26	100.0	575	1 HEMA_SENDJ	P06863 sendai viru
17	26	100.0	575	1 HEMA_SENDZ	P04853 sendai viru
18	26	100.0	576	1 HEMA_SENDH	P03425 sendai viru
19	26	100.0	581	1 MK1_SCHPO	P30290 schizosacch
20	26	100.0	644	1 YEAG_ECOLI	P77391 escherichia
21	26	100.0	676	1 UL06_HSV11	P01090 herpes simp
22	26	100.0	687	1 PKP_ECOLI	P28688 escherichia
23	26	100.0	687	1 PKP_SALTY	O85090 salmonella
24	26	100.0	738	1 MAS2_CORGL	P42450 corynebacte
25	26	100.0	778	1 SEA2_MYCLE	O32922 mycobacteri
26	26	100.0	808	1 SEA2_MYCTU	Q50612 mycobacteri
27	26	100.0	1071	1 CARB_BACSU	P25994 bacillus su
28	26	100.0	1295	1 BXAL_CLOBO	P10845 clostridium
29	26	100.0	1295	1 BXA2_CLOBO	Q45894 clostridium
30	26	100.0	2061	1 MYOF_HUMAN	Q9nzm1 homo sapien
31	25	96.2	10	1 ANGI_BOTJA	Q10581 bothrops ja
32	25	96.2	10	1 ANGT_BOVIN	P01017 bos taurus
33	25	96.2	10	1 ANGT_CHICK	P01018 gallus gall

34	25	96.2	114	1 MIF_BOVIN	P80177 bos taurus
35	25	96.2	114	1 MIF_MERUN	O55052 meriones un
36	25	96.2	178	1 BDH_BOVIN	Q02337 bos taurus
37	25	96.2	272	1 PK1_NPVAC	P41415 autographa
38	25	96.2	311	1 NFE2_RHIME	Q52994 rhizobium m
39	25	96.2	446	1 GGAA_BACSU	P46917 bacillus su
40	25	96.2	465	1 YC14_KLEPN	Q04660 lactobacill
41	25	96.2	488	1 GAL7_LACHE	Q00054 lactobacill
42	25	96.2	511	1 EGO_ECOLI	P77257 escherichia
43	25	96.2	539	1 PRIS_METJA	O58175 methanococc
44	25	96.2	572	1 HEMA_PI3B	P08167 bovine para
45	25	96.2	574	1 CDAS_THET	P29964 thermoanaer

ALIGNMENTS

RESULT 1  
ANG2\_BOTJA  
ID ANG2\_BOTJA STANDARD; PRT; 8 AA.  
AC O10582;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide II (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
RT "Isolation and identification of angiotensin-like peptides from the  
plasma of the snake Bothrops jararaca."  
RL Comp. Biochem. Physiol. 113B:467-473(1996).  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro; IPR000215; Serpin.  
KW PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 26; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
| | | | |  
DB 1 DRVYI 5

RESULT 2  
ANGT\_HORSE  
ID ANGT\_HORSE STANDARD; PRT; 14 AA.  
AC P01016;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen (Contains: Angiotensin I; Angiotensin II) (Fragment).  
GN SERPIN8 OR Act.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE.  
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;  
RT "The preparation, purification, and amino acid sequence of a  
polypeptide renin substrate.";

RL J. Exp. Med. 106:439-453(1957).  
CC -|- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -|- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
CC PIR: A01250; A01250.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBDD7 CRC64;  
  
Query Match 100.0%; Score 26; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVYI 5  
| | | | |  
DB 1 DRVYI 5  
  
RESULT 3  
MIF\_CHICK STANDARD; PRT; 114 AA.  
ID MIF\_CHICK  
AC Q02960;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate  
DE tautomerase).  
GN MIF.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lens;  
RX MEDLINE=93165679; PubMed=7679497;  
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;  
RT "A macrophage migration inhibitory factor is expressed in the  
RT differentiating cells of the eye lens."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).  
CC -|- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A  
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN  
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.  
CC -|- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO THE MIF FAMILY.  
-----  
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-----  
DR EMBL; M95776; AAA48939.1; --  
DR PIR; C47274; C47274.  
DR HSP; P34884; IMFI.  
DR InterPro: IPR001398; MIF.  
DR Pfam: PF01187; MIF; 1.  
DR PROSITE; PS01158; MIF; 1.  
KW Isomerase; Macrophage; Inflammatory response; Cytokine.  
FT ACT\_SITE 1 1 CATALYTIC BASE (BY SIMILARITY).

FT INIT\_MET 0 0 BY SIMILARITY.  
SQ SEQUENCE 114 AA; 12353 MW; A55222D00E6D05CF CRC64;  
  
Query Match 100.0%; Score 26; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVYI 5  
| | | | |  
DB 92 DRVYI 96  
  
RESULT 4  
MIF\_HUMAN STANDARD; PRT; 114 AA.  
ID MIF\_HUMAN  
AC P14174;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate  
DE tautomerase) (Glycosylation-inhibiting factor) (GIF).  
GN MIF OR MMIF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90017510; PubMed=2552447;  
RA Weiser W.Y., Temple P.A., Witek-Giannotti J.S., Remold H.G.,  
RA Clark S.C., David J.R.;  
RT "Molecular cloning of a cDNA encoding a human macrophage migration  
RT inhibitory factor."  
RL Proc. Natl. Acad. Sci. U.S.A. 86:7522-7526(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94245178; PubMed=8188240;  
RA Paralkar V., Wistow G.J.;  
RT "Cloning the human gene for macrophage migration inhibitory factor  
RT (MIF)."  
RL Genomics 19:48-51(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94052102; PubMed=8234256;  
RA Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C.,  
RA Iwamatsu A., Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;  
RT "Molecular cloning and functional expression of a cDNA encoding  
RT glycosylation-inhibiting factor."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).  
RN [4]  
RP SEQUENCE OF 9-114 FROM N.A.  
RC TISSUE=Lens;  
RX MEDLINE=93165679; PubMed=7679497;  
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;  
RT "A macrophage migration inhibitory factor is expressed in the  
RT differentiating cells of the eye lens."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).  
RN [5]  
RP SEQUENCE OF 1-10.  
RC TISSUE=Liver;  
RX MEDLINE=93162045; PubMed=1286669;  
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
RA Appel R.D., Hughes G.J.;  
RT "Human liver protein map: a reference database established by  
RT microsequencing and gel comparison."  
RL Electrophoresis 13:992-1001(1992).  
RN [6]  
RP SEQUENCE OF 2-23.  
RX MEDLINE=93256574; PubMed=7683862;  
RA Zeng F.Y., Weiser W.Y., Kratzin H., Stahl B., Karas M., Gubius H.J.;  
RT "The major binding protein of the interferon antagonist sarcolectin



in human placenta is a macrophage migration inhibitory factor.";

RL Arch. Biochem. Biophys. 303:74-80(1993).  
[7]  
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RA Sugimoto H., Suzuki M., Nakagawa A., Tanaka I., Nishihira J.;  
RT "Crystal structure of macrophage migration inhibitory factor from  
human lymphocyte at 2.1-A resolution.";  
RL FEBS Lett. 389:145-148(1996).  
[8]  
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RX MEDLINE-96181524; PubMed-8610159;  
RA Kato Y., Muto T., Tomura T., Tsumura H., Watarai H., Mikayama T.,  
RA Ishizaka K., Kuroki R.;  
RT "The crystal structure of human glycosylation-inhibiting factor is a  
trimeric barrel with three 6-stranded beta-sheets.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:3007-3010(1996).  
[9]  
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RX MEDLINE-96224258; PubMed-8643551;  
RA Sun H.W., Bernhagen J., Bucala R., Lolis E.;  
RT "Crystal structure at 2.6-A resolution of human macrophage migration  
inhibitory factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:5191-5196(1996).  
[10]  
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE-99282199; PubMed-10353846;  
RA Lubetsky J.B., Swope M., Dealwis C., Blake P., Lolis E.;  
RT "Pro-1 of macrophage migration inhibitory factor functions as a  
catalytic base in the phenylpyruvate tautomerase activity.";  
RL Biochemistry 38:7346-7354(1999).  
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A  
ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN  
HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.  
CC -!- SUBUNIT: HOMOTRIMER.  
CC -!- DISEASE: MIF ACTIVITY HAS BEEN DETECTED IN LEUKOCYTE CULTURE  
SUPERNATANTS OF MICE DURING ALLOGRAFT REJECTION, IN THE SYNOVIA  
OF PATIENTS WITH RHEUMATOID POLYARTHRITIS, AND IN A VARIETY OF  
CHRONIC INFLAMMATORY LOCII.  
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.  
-----  
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-----  
DR EMBL; 223063; CAA80598.1; -  
DR EMBL; M25639; AAA36315.1; -  
DR EMBL; M95775; AAA36179.1; -  
DR EMBL; L10612; AAA35892.1; -  
DR EMBL; L19686; AAA21814.1; -  
DR PIR; A33838; A33838.  
DR PIR; S33277; S33277.  
DR PDB; 1GIF; 12-MAR-97.  
DR PDB; 1MIF; 07-DEC-96.  
DR PDB; 1P1G; 07-JUN-99.  
DR PDB; 1CGQ; 07-JUN-99.  
DR PDB; 1CA7; 30-JUN-99.  
DR SWISS-2DPAGE; P14174; HUMAN.  
DR Sien-2DPAGE; P14174; -  
DR MIM; 153620; -  
DR InterPro; IPR001398; MIF.  
DR Pfam; PF01187; MIF; 1.  
DR PROSITE; PS01158; MIF; 1.  
KW Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.  
FT INIT\_MET 0  
FT ACT\_SITE 1 CATALYTIC BASE.  
FT ACT\_SITE 105 105 N -> S (IN REF. 1).  
FT CONFLICT 114 AA; 12345 MW; 4BD525232B3F3069 CRC64;  
SQ SEQUENCE

Query Match 100.0%; Score 26; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 92 DRVYI 96  
|||||

RESULT 5  
MIF\_MOUSE  
ID MIF\_MOUSE STANDARD; PRT; 114 AA.  
AC P34884;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate  
DE tautomerase) (Delayed early response protein 6) (DER6) (Glycosylation-  
DE inhibiting factor).  
GN MIF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.  
RC TISSUE=Pituitary;  
RX MEDLINE-94019845; PubMed-8413654;  
RA Bernhagen J., Calandra T., Mitchell R.A., Martin S.B.,  
RA Tracey K.J., Voelter W., Manogue K.R., Cerami A., Bucala R.;  
RT "MIF is a pituitary-derived cytokine that potentiates lethal  
RT endotoxaemia.";  
RL Nature 365:756-759(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/C;  
RX MEDLINE-92375060; PubMed-1508193;  
RA Lanahan A., Williams J.B., Sanders L.K., Nathans D.;  
RT "Growth factor-induced delayed early response genes.";  
RL Mol. Cell. Biol. 12:3919-3929(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-94052102; PubMed-8234256;  
RA Miyama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C., Iwamatsu A.,  
RA Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;  
RT "Molecular cloning and functional expression of a cDNA encoding  
RT glycosylation-inhibiting factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RX MEDLINE-95221891; PubMed-7706726;  
RA Mitchell R., Bacher M., Bernhagen J., Pushkarskaya T., Seldin M.F.,  
RA Bucala R.;  
RT "Cloning and characterization of the gene for mouse macrophage  
RT migration inhibitory factor (MIF).";  
RL J. Immunol. 154:3863-3870(1995).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RX MEDLINE-96047325; PubMed-7558021;  
RA Bozza M., Kolakowski L.F. Jr., Jenkins N.A., Gilbert D.J.,  
RA Copeland N.G., David J.R., Gerard C.;  
RT "Structural characterization and chromosomal location of the mouse  
RT macrophage migration inhibitory factor gene and pseudogenes.";  
RL Genomics 27:412-419(1995).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RX MEDLINE-96047324; PubMed-7558020;  
RA Kozak C.A., Adamson M.C., Buckler C.E., Segovia L., Paralkar V.,  
RA Wistow G.;

\*Genomic cloning of mouse MIF (macrophage inhibitory factor) and genetic mapping of the human and mouse expressed gene and nine mouse pseudogenes.";  
Genomics 27:405-411(1995).  
[7]  
RP SEQUENCE OF 5-114 FROM N.A.  
RC TISSUE=Lens;  
RX MEDLINE=93165679; PubMed=7679497;  
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;  
RT "A macrophage migration inhibitory factor is expressed in the differentiating cells of the eye lens.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
RX MEDLINE=99303983; PubMed=10360941;  
RA Taylor A.B., Johnson W.H. Jr., Czerwinski R.M., Li H.S., Hackert M.L., Whitman C.P.;  
RT "Crystal structure of macrophage migration inhibitory factor complexed with (E)-2-fluoro-p-hydroxycinnamate at 1.8 A resolution: implications for enzymatic catalysis and inhibition.";  
RL Biochemistry 38:7444-7452(1999).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS).  
RX MEDLINE=20393856; PubMed=10933783;  
RA Stamps S.L., Taylor A.B., Wang S.C., Hackert M.L., Whitman C.P.;  
RT "Mechanism of the phenylpyruvate tautomerase activity of macrophage migration inhibitory factor: properties of the PIG, P1A, Y95F, and N97A mutants.";  
RL Biochemistry 39:9671-9678(2000).  
CC -1- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN HOST DEFENSE. ALSO ACTS AS A PHENYLPIYRUVATE TAUTOMERASE.  
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE MIF FAMILY.  
CC -----  
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CC -----  
CC EMBL; 223048; CAA80583.1; -;  
CC EMBL; U19825; AAA91637.1; -;  
CC EMBL; L10613; AAA37693.1; -;  
CC EMBL; U20156; AAA91638.1; -;  
CC EMBL; L39357; AAA74321.1; -;  
CC EMBL; L07607; AAA37111.1; -;  
CC PIR; S34299; S34299.  
CC PIR; A44499; A44499.  
CC PDB; 1MFF; 11-AUG-00.  
CC PDB; 1MFI; 22-JUN-99.  
CC MGD; MGI:96982; Mif.  
CC InterPro; IPR001398; MIF.  
CC Pfam; PF01187; MIF; 1.  
CC PROSITE; PS01158; MIF; 1.  
CC Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.  
FT INIT\_MET 0 0 CATALYTIC BASE.  
SQ SEQUENCE 114 AA; 12373 MW; 8FD2339CF0792F9E CRC64;  
  
Query Match 100.0%; Score 26; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DRVYI 5  
| | | | |  
Db 92 DRVYI 96  
  
RESULT 6

MIF\_RAT  
ID MIF\_RAT STANDARD; PRT; 114 AA.  
AC P30904;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (Glutathione-binding 13 kDa protein).  
DE DE tautomerase)  
GN MIF.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=101116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95038523; PubMed=7951062;  
RA Sakai M., Nishihira J., Hibiya Y., Koyama Y., Nishi S.;  
RT "Glutathione binding rat liver 13k protein is the homologue of the macrophage migration inhibitory factor.";  
RL Biochem. Mol. Biol. Int. 33:439-446(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lens;  
RA Wen Y., Li G., Bekhor I.;  
RN Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PVG/C;  
RA Sleeman M.A., Huckle J.W., Robinson M., Jahoda C.A.B., Reynolds A.J., Whitehouse C.J.;  
RN Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-25.  
RX MEDLINE=93063370; PubMed=1436109;  
RA Blocki F.A., Schlievert P.M., Wackett L.P.;  
RT "Rat liver protein linking chemical and immunological detoxification systems.";  
RL Nature 360:269-270(1992).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RC TISSUE=Liver;  
RX MEDLINE=96186248; PubMed=8605628;  
RA Suzuki M., Sugimoto H., Nakagawa A., Tanaka I., Nishihira J., Sakai M.;  
RT "Crystal structure of the macrophage migration inhibitory factor from rat liver.";  
RL Nat. Struct. Biol. 3:259-266(1996).  
CC -1- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN HOST DEFENSE. ALSO ACTS AS A PHENYLPIYRUVATE TAUTOMERASE.  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF ORGANS INCLUDING BRAIN, SPLEEN, LIVER, MUSCLE AND KIDNEY.  
CC -1- SIMILARITY: BELONGS TO THE MIF FAMILY.  
CC -----  
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CC -----  
CC EMBL; S73424; AAB32392.1; -;  
CC EMBL; U20999; AAA62644.1; -;  
CC EMBL; U62326; AAB04024.1; -;  
CC PDB; 1FIM; 11-JUL-96.  
CC InterPro; IPR001398; MIF.  
CC Pfam; PF01187; MIF; 1.  
CC PROSITE; PS01158; MIF; 1.  
CC Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.  
FT INIT\_MET 0 0

FT ACT\_SITE 1 1 CATALYTIC BASE (BY SIMILARITY).  
FT CONFLICT 50 50 S -> R (IN REF. 2).  
SQ SEQUENCE 114 AA; 12346 MW; 9E33C39CF064329E CRC64;

Query Match 100.0%; Score 26; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 92 DRVYI 96

## RESULT 7

TXB6\_HUMAN  
ID TXB6\_HUMAN STANDARD; PRT: 436 AA.  
AC O95947;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX6 (T-box protein 6).  
GN TBX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99134303; PubMed=9933572;  
RA Papapetrou C., Putt W., Fox M., Edwards Y.H.;  
RT "The human TBX6 gene: Cloning and assignment to chromosome 16p11.2.";  
RL Genomics 55:238-241(1999).  
RN [2]  
RP SEQUENCE OF 135-272 FROM N.A.  
RC TISSUE=Myeloid;  
RX MEDLINE=99107806; PubMed=9888994;  
RA Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,  
RA Armstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;  
RT "Identification, mapping and phylogenomic analysis of four new human  
members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";  
RL Genomics 55:10-20(1999).  
CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN  
DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF  
PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).  
CC -!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).  
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL  
TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT  
TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.  
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A  
SECOND PHASE IN SOME ADULT TISSUES.  
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; AJ007989; CAA07812.1;  
DR EMBL; AJ010279; CAB37938.1;  
DR HSSP; P24781; 1XB8.  
DR MIM; 602427;  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF005907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.

KW Transcription regulation; DNA-binding; Nuclear protein;  
KW Developmental protein.  
FT DNA\_BIND 100 273 T-BOX  
FT CONFLICT 207 207 H -> HV (IN REF. 2).  
SQ SEQUENCE 436 AA; 47017 MW; 438178BD31B966E9 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 170 DRVYI 174

## RESULT 8

ANGT\_SHEEP  
ID ANGT\_SHEEP STANDARD; PRT: 476 AA.  
AC P20757;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPIN A8 OR AGT.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95072318; PubMed=7765514;  
RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,  
RA Murakami K., Nakamura Y.;  
RT "Sequencing and expression of sheep angiotensinogen cDNA.";  
RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).  
RN [2]  
RP SEQUENCE OF 25-39.  
RX MEDLINE=86136099; PubMed=3081342;  
RA Fernley R.T., John M., Niall H.D., Coghlan J.P.;  
RT "Purification and characterization of ovine angiotensinogen.";  
RL Eur. J. Biochem. 154:597-601(1986).  
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CLEASES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
BALANCE OF BODY FLUIDS.  
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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DR EMBL; D17520; BAA04470.1;  
DR PIR; A25406; A25406.  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Vasocostrictor; Glycoprotein; Plasma; Serpin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 476 ANGIOTENSINOGEN.  
FT PEPTIDE 25 34 ANGIOTENSIN I.

FT PEPTIDE 25 32 ANGIOTENSIN II.  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 25 DRVYI 29  
|||||

RESULT 9  
ANGT\_MOUSE STANDARD; PRT; 477 AA.  
AC P11859;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPIN A8 OR AGT.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88284703; PubMed=3397061;  
RA Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;  
RT "Molecular cloning of the mouse angiotensinogen gene.";  
RL Genomics 2:240-248(1988).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; AF045887; AAC01765.1;  
DR EMBL; AF045886; AAC01765.1; JOINED.  
DR EMBL; AF045885; AAC01765.1; JOINED.  
DR EMBL; AF045884; AAC01765.1; JOINED.  
DR PIR; A29978; A29978.  
DR MGD; MGI:87963; Agt.  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; FALSE\_NEG.  
KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 477 ANGIOTENSINOGEN.  
FT PEPTIDE 25 34 ANGIOTENSIN I.  
FT PEPTIDE 25 32 ANGIOTENSIN II.  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 477 AA; 51990 MW; A677F4029F338607 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 25 DRVYI 29  
|||||

RESULT 10  
ANGT\_RAT STANDARD; PRT; 477 AA.  
AC P01015;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPIN A8 OR AGT.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR;  
RX MEDLINE=83159849; PubMed=6572971;  
RA Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.;  
RT "Cloning and sequence analysis of cDNA for rat angiotensinogen.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).  
RN [2]  
RP SEQUENCE OF 25-34.  
RX MEDLINE=73060322; PubMed=4344907;  
RA Nakayama T., Nakajima T., Sokabe H.;  
RT "Comparative studies on angiotensins. II. Structure of rat  
RT angiotensin and its identification by DNS-method.";  
RL Chem. Pharm. Bull. 20:1579-1581(1972).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
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CC -----  
DR EMBL; L00094; AAA98779.1;  
DR EMBL; L00091; AAA98779.1; JOINED.  
DR EMBL; L00092; AAA98779.1; JOINED.  
DR EMBL; L00093; AAA98779.1; JOINED.  
DR PIR; A01251; ANET.  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; FALSE\_NEG.  
KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 477 ANGIOTENSINOGEN.  
FT PEPTIDE 25 34 ANGIOTENSIN I.  
FT PEPTIDE 25 32 ANGIOTENSIN II.  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 477 AA; 51981 MW; 689051A5788D693D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 25 DRVYI 29

RESULT 11  
ANGT\_HUMAN  
ID ANGT\_HUMAN STANDARD; PRT; 485 AA.  
AC P01019; Q16358; Q16359;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPIN A8 OR AGT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=89170129; PubMed=2924688;  
RA Gaillard I., Clauser E., Corvol P.;  
RT "Structure of human angiotensinogen gene.";  
RL DNA 8:87-99(1989).  
[2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=85000455; PubMed=6089875;  
RA Kageyama R., Ohkubo H., Nakanishi S.;  
RT "Primary structure of human preangiotensinogen deduced from the  
cloned cDNA sequence.";  
RL Biochemistry 23:3603-3609(1984).  
[3]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=90237063; PubMed=1692023;  
RA Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,  
RA Murakami K.;  
RT "Structure and expression of the human angiotensinogen gene.  
Identification of a unique and highly active promoter.";  
RL J. Biol. Chem. 265:7576-7582(1990).  
[4]  
RN SEQUENCE OF 1-338 FROM N.A.  
RP MEDLINE=87244745; PubMed=2885106;  
RA Kunapuli S.P., Kumar A.;  
RT "Molecular cloning of human angiotensinogen cDNA and evidence for the  
presence of its mRNA in rat heart.";  
RL Circ. Res. 60:786-790(1987).  
[5]  
RN SEQUENCE OF 34-45, AND SUBUNITS.  
RC TISSUE-Serum;  
RX MEDLINE=95293954; PubMed=7539791;  
RA Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,  
RA Stigbrand T., Gleich G.J., Sottrup-Jensen L.;  
RT "Identification of angiotensinogen and complement C3dg as novel  
proteins binding the proform of eosinophil major basic protein in  
human pregnancy serum and plasma.";  
RL J. Biol. Chem. 270:13645-13651(1995).  
[6]  
RN SEQUENCE OF 34-43.  
RP MEDLINE=69014170; PubMed=4300938;  
RA Arakawa K., Minohara A., Yamada J., Nakamura M.;  
RT "Enzymatic degradation and electrophoresis of human angiotensin I.";  
RL Biochim. Biophys. Acta 168:106-112(1968).  
[7]  
RN STRUCTURE BY NMR OF ANGIOTENSIN II.  
RP MEDLINE=98151281; PubMed=9492317;  
RA Carpenter K.A., Wilkes B.C., Schaller P.W.;  
RT "The octapeptide angiotensin II adopts a well-defined structure in a

phospholipid environment.";  
RL Eur. J. Biochem. 251:448-453(1998).  
[8]  
RN VARIANTS MET-207; THR-268 AND CYS-281.  
RX MEDLINE=93008239; PubMed=1394429;  
RA Jeunenaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,  
RA Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,  
RA Lalouel J.-M., Corvol P.;  
RT "Molecular basis of human hypertension: role of angiotensinogen.";  
RL Cell 71:169-180(1992).  
[9]  
RN VARIANT THR-268.  
RX MEDLINE=93291876; PubMed=8513325;  
RA Ward K., Hata A., Jeunenaitre X., Helin C., Nelson L., Namikawa C.,  
RA Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,  
RA Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;  
RT "A molecular variant of angiotensinogen associated with  
preeclampsia.";  
RL Nat. Genet. 4:59-61(1993).  
[10]  
RN VARIANTS ILE-242; ARG-244 AND CYS-281.  
RX MEDLINE=95331754; PubMed=7607642;  
RA Hixson J.E., Powers P.K.;  
RT "Detection and characterization of new mutations in the human  
angiotensinogen gene (AGT).";  
RL Hum. Genet. 96:110-112(1995).  
[11]  
RN FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
BALANCE OF BODY FLUIDS.  
[12]  
RN SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2  
heterodimer with the proform of PRG2 and as a complex (probably  
a 2:2:2 heterotrimer) with pro-PRG2 and C3dg.  
[13]  
RN TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
[14]  
RN DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO  
ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION  
(PIH) (PREECLAMPSIA).  
[15]  
RN SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
[16]  
RN CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.  
[17]  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
[18]  
RN EMBL; K02215; AAA51731.1; -  
DR EMBL; M24689; AAA51679.1; -  
DR EMBL; M24686; AAA51679.1; JOINED.  
DR EMBL; M24687; AAA51679.1; JOINED.  
DR EMBL; M24688; AAA51679.1; JOINED.  
DR EMBL; X15324; CAA33385.1; -  
DR EMBL; X15325; CAA33385.1; JOINED.  
DR EMBL; X15326; CAA33385.1; JOINED.  
DR EMBL; X15327; CAA33385.1; JOINED.  
DR EMBL; M69110; AAA52282.1; -  
DR EMBL; S78529; AAD14287.1; -  
DR EMBL; S78530; AAD14288.1; -  
DR PIR; A01249; ANHU.  
DR PIR; A31362; A31362.  
DR PIR; A35203; A35203.  
DR SWISS-2DPAGE; P01019; HUMAN.  
DR MIM; 106150; -  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.

KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;  
KW Disease mutation; Polymorphism.  
FT SIGNAL 1 33  
FT CHAIN 34 485  
FT PEPTIDE 34 41 ANGIOTENSINOGEN.  
FT PEPTIDE 34 41 ANGIOTENSIN I.  
FT CARBOHYD 47 47 ANGIOTENSIN II.  
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 207 207 T -> M.  
FT VARIANT 242 242 /FTid=VAR\_007093.  
FT VARIANT 244 244 T -> I (IN HYPERTENSION).  
FT VARIANT 244 244 L -> R (IN HYPERTENSION).  
FT VARIANT 268 268 /FTid=VAR\_007095.  
FT VARIANT 268 268 M -> T (IN HYPERTENSION).  
FT VARIANT 281 281 /FTid=VAR\_007096.  
FT VARIANT 281 281 Y -> C (IN HYPERTENSION).  
FT VARIANT 333 333 /FTid=VAR\_007097.  
FT CONFLICT 333 333 O -> E (IN REF. 1).  
FT SEQUENCE 485 AA; 53154 MW; 5026C2DFB2DD236E CRC64;

Query Match 100.0%; Score 26; DB 1; Length 485;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
DB 34 DRVYI 38

RESULT 12  
YB95\_METJA

ID YB95\_METJA STANDARD; PRT; 518 AA.  
AC Q58595;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Putative 2-isopropylmalate/homocitrate synthase MJ1195 (EC 4.1.3.-).  
GN MJ1195.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
OX Methanococcus.  
OX NCBI\_TaxID=2190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
RX MEDLINE=96337999; PubMed=8688087;  
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";  
RL Science 273:1058-1073(1996).

CC -1- SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE / HOMOCITRATE  
CC SYNTHASE FAMILY.

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CC EMBL; U67561; AAB99199.1; -

DR TIGR; MJ1195;  
DR InterPro: IPR002034; AIPM\_homocit\_synth.  
DR InterPro: IPR000891; HMGL-like.  
DR Pfam: PF00682; HMGL-like; 1.  
DR PROSITE: PS00815; AIPM\_HOMOCIT\_SYNTH\_1; 1.  
DR PROSITE: PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1.  
KW Hypothetical protein; Lyase; Complete proteome.  
SQ SEQUENCE 518 AA; 56620 MW; 604AB61B41E607A4 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 518;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
DB 22 DRVYI 26

RESULT 13

TBX6\_MOUSE  
ID TBX6\_MOUSE STANDARD; PRT; 540 AA.  
AC P70327;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX6 (T-box protein 6).  
GN TBX6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=97032942; PubMed=8878690;  
RA Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,  
RA Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;  
RT "Evolution of mouse T-box genes by tandem duplication and cluster  
RT dispersion.";  
RL Genetics 144:249-254(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Gastrula;  
RX MEDLINE=97115702; PubMed=8954725;  
RA Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;  
RT "Tbx6, a mouse T-box gene implicated in paraxial mesoderm formation at  
RT gastrulation.";  
RL Dev. Biol. 180:534-542(1996).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=98140705; PubMed=9490412;  
RA Chapman D.L., Papaioannou V.E.;  
RT "Three neural tubes in mouse embryos with mutations in the T-box gene  
RT Tbx6.";  
RL Nature 391:695-697(1998).  
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN  
CC DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL  
CC MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS  
CC DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL  
CC PATHWAY.  
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -1- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION  
CC STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL  
CC MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,  
CC PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK  
CC AS THE SOURCE OF MESODERM.  
CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

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CC EMBL; U57331; AAC53110.1; -;  
DR HSSP; P24781; LXBR.  
DR MGD; MGI:102539; Tbx6.  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein;  
KW Developmental protein.  
FT DOMAIN 61 64 POLY-ALA.  
FT DOMAIN 79 82 POLY-PRO.  
FT DNA\_BIND 100 273 T-BOX.  
SQ SEQUENCE 540 AA; 58628 MW; BC834CE2745E8E61 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 540;

Best Local Similarity 100.0%; Pred. No. 66;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 170 DRVYI 174

RESULT 14

HEMA\_SENDS STANDARD; PRT; 575 AA.

AC P27562;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemagglutinin-neuraminidase (EC 3.2.1.18).

GN HN.

OS Sendai virus (strain Z / host mutants).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.

OX NCBI\_TaxID=11192;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MUTANT JS-F1, AND MUTANT F1-R;

RX MEDLINE=90266486; PubMed=2161155;

RA Middleton Y., Tashiro M., Thai T., Oh J., Seymour J., Pritzner E.,

RA Klenk H.D., Rott R., Seto J.T.;

RT "Nucleotide sequence analyses of the genes encoding the HN, M, NP, P,

RT and L proteins of two host range mutants of Sendai virus.";

RL Virology 176:656-657(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=MUTANT F1-R / T-5 REVERTANT;

RX MEDLINE=91335752; PubMed=1651590;

RA Tashiro M., James I., Karri S., Wahn K., Tobita K., Klenk H.D.,

RA Rott R., Seto J.T.;

RT "Pneumotropic revertants derived from a pantropic mutant, F1-R, of

RT Sendai virus.";

RL Virology 184:227-234(1991).

CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS

CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE

CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING

CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING

CC GLYCOPROTEINS.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,

CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in

CC oligosaccharides, glycoproteins, glycolipids, colominic acid and

CC synthetic substrates.

CC -!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS

CC -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
CC NEURAMINIDASE FAMILY.  
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CC EMBL; M30202; AAB06282.1; -;

DR EMBL; M30203; AAB06288.1; -;

DR EMBL; M30204; AAB06200.1; -;

DR EMBL; M69046; AAB06294.1; -;

DR InterPro; IPR000665; Hem-neuramidase.

DR Pfam; PF00423; HN; 1.

KW Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;

KW Transmembrane.

FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 60 POTENTIAL.

FT DOMAIN 61 575 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 575 AA; 63469 MW; 86EE5B73AD7EB2D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 575;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 419 DRVYI 423

RESULT 15

HEMA\_SENDF

ID HEMA\_SENDF STANDARD; PRT; 575 AA.

AC P19758;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemagglutinin-neuraminidase (EC 3.2.1.18).

GN HN.

OS Sendai virus (strain Fushimi).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.

OX NCBI\_TaxID=11195;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91057133; PubMed=2173829;

RA Neubert W.J., Willenbrink W.;

RT "Cloning and sequencing of the HN gene of Sendai virus (strain

RT Fushimi).";

RL Nucleic Acids Res. 18:6427-6427(1990).

CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS

CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE

CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING

CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING

CC GLYCOPROTEINS.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,

CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in

CC oligosaccharides, glycoproteins, glycolipids, colominic acid and

CC synthetic substrates.

CC -!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS

CC N-TERMINAL HYDROPHOBIC SEQUENCE.

CC -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-

CC NEURAMINIDASE FAMILY.  
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DR EMBL; X56131; CAA39596.1; -  
 DR PIR; S12135; S12135.  
 DR PIR; S12462; S12462.  
 DR InterPro: IPR000665; Hem-neuramndse.  
 DR Pfam: PF00423; HN; 1.  
 KW Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;  
 KW Transmembrane.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 60 POTENTIAL.  
 FT DOMAIN 61 575 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 575 AA; 63347 MW; 93FD0532F6147BF6 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYI 5  
 |||||  
 Db 419 DRVYI 423

Search completed: July 1, 2002, 07:47:09  
 Job time: 475 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:13 ; Search time 122.73 Seconds  
(without alignments)  
7.048 Million cell updates/sec

Title: US-09-723-197-9

Perfect score: 26

Sequence: 1 DRVYI 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	100.0	14	5 Q10757	Q10757 theromyzon
2	26	100.0	72	2 Q9R540	Q9R540 clostridium
3	26	100.0	87	8 Q9G9H0	Q9G9H0 eretmoceru
4	26	100.0	167	16 Q9KG21	Q9KG21 bacillus ha
5	26	100.0	173	12 Q88184	Q88184 san miguel
6	26	100.0	178	17 Q9HIS3	Q9HIS3 thermoplasm
7	26	100.0	186	5 Q9W387	Q9W387 drosophila
8	26	100.0	195	17 Q28741	Q28741 archaeglob
9	26	100.0	199	17 Q973E6	Q973E6 sulfolobus
10	26	100.0	238	16 Q66729	Q66729 aquifex aeo
11	26	100.0	245	6 Q95J13	Q95J13 pan troglod
12	26	100.0	248	2 Q44326	Q44326 agrobacteri
13	26	100.0	291	3 Q9C445	Q9C445 penicillium
14	26	100.0	291	4 Q9HBV1	Q9HBV1 homo sapien
15	26	100.0	291	11 Q9ES81	Q9ES81 mus musculu
16	26	100.0	295	4 Q9HA44	Q9HA44 homo sapien

17	26	100.0	300	10 Q94JW3	Q94JW3 arabidopsis
18	26	100.0	312	10 Q48726	Q48726 arabidopsis
19	26	100.0	321	5 Q9GNL3	Q9GNL3 drosophila
20	26	100.0	340	12 Q9DVM3	Q9DVM3 plutella xy
21	26	100.0	369	13 Q9IAE7	Q9IAE7 pantodon bu
22	26	100.0	377	13 Q9IAG5	Q9IAG5 gymmarchus
23	26	100.0	408	10 Q9MA64	Q9MA64 arabidopsis
24	26	100.0	409	17 Q27084	Q27084 methanother
25	26	100.0	419	17 Q973T1	Q973T1 sulfolobus
26	26	100.0	448	10 Q94F16	Q94F16 arabidopsis
27	26	100.0	461	11 Q9D2V0	Q9D2V0 mus musculu
28	26	100.0	477	4 Q96FD5	Q96FD5 homo sapien
29	26	100.0	485	4 Q96F91	Q96F91 homo sapien
30	26	100.0	485	6 Q9GLP7	Q9GLP7 pan troglod
31	26	100.0	485	6 Q9GLP6	Q9GLP6 gorilla gor
32	26	100.0	485	6 Q9GLN8	Q9GLN8 pan troglod
33	26	100.0	486	6 Q9TFS20	Q9TFS20 callithrix
34	26	100.0	486	13 Q90XI3	Q90XI3 chiloscylli
35	26	100.0	509	10 Q9T0L4	Q9T0L4 arabidopsis
36	26	100.0	509	10 Q94AR8	Q94AR8 arabidopsis
37	26	100.0	575	12 Q88413	Q88413 sendai viru
38	26	100.0	584	16 Q97H15	Q97H15 clostridium
39	26	100.0	614	2 Q87250	Q87250 lactococcus
40	26	100.0	644	16 Q9KQX5	Q9KQX5 vibrio chol
41	26	100.0	661	16 Q9KCM3	Q9KCM3 bacillus ha
42	26	100.0	749	16 P73687	P73687 synechocyst
43	26	100.0	798	2 Q9E2L3	Q9E2L3 mycobacteri
44	26	100.0	800	2 Q93C65	Q93C65 thermus aqu
45	26	100.0	838	3 Q94653	Q94653 schizosacch

ALIGNMENTS

RESULT 1

ID	Q10757	PRELIMINARY;	PRT;	14	AA.
AC	Q10757;				
DT	01-NOV-1996	(TREMBLrel. 01, Created)			
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			
DE	01-NOV-1998	(TREMBLrel. 08, Last annotation update)			
DE	ANGIOTENSINOGEN (FRAGMENT).				
OS	Theromyzon tessulatum (Leech).				
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;				
OC	Rhynchobdellida; Glossiphoniidae; Theromyzon.				
OX	NCBI_TaxID=13286;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=95365039; PubMed=7637887;				
RA	Laurent V., Bulet P., Salzet M.A.;				
RT	"A comparison of the leech Theromyzon tessulatum angiotensin I-like				
RT	molecule with forms of vertebrate angiotensinogens: a hormonal system				
RL	conserved in the course of evolution.";				
RL	Neurosci. Lett. 190:175-178(1995).				
RN	[2]				
RP	SEQUENCE OF 1-10.				
RC	TISSUE=BRAIN;				
RX	MEDLINE=96201949; PubMed=8612806;				
RA	Laurent V., Salzet M.;				
RT	"Metabolism of angiotensins by head membranes of the leech Theromyzon				
RT	tessulatum.";				
RL	FEBS Lett. 384:123-127(1996).				
CC	-I- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.				
KW	Glycoprotein; Serpin.				
FT	NON_TER 14 14				
SQ	SEQUENCE 14 AA; 1763 MW; 335109D8EEFDD7 CRC64;				

Query Match 100.0%; Score 26; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYI 5

Db 1 DRVYI 5  
|||||

RESULT 2  
Q9R540 PRELIMINARY; PRT; 72 AA.  
ID Q9R540  
AC Q9R540;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE NEUROTOXIN HEAVY CHAIN 18 KDA FRAGMENT (FRAGMENT).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94000342; PubMed=8397793;  
RA Gimenez J.A., DasGupta B.R.;  
RT "Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72,  
RT 45, 42, and 18 kD fragments.";  
RL J. Protein Chem. 12:351-363(1993).  
DR HSSP: P10845; 3BPA.  
SQ SEQUENCE 72 AA; 8165 MW; B7A959576A615E18 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||

Db 31 DRVYI 35

RESULT 3  
Q9G9H0 PRELIMINARY; PRT; 87 AA.  
ID Q9G9H0  
AC Q9G9H0;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE CYTOCHROME OXIDASE II (FRAGMENT).  
OS Eretmococcus mundus.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
OC Chalcidoidea; Aphelinidae; Eretmocerus.  
OX NCBI\_TaxID=77302;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA De Barro P.J., Driver F., Naumann I.D., Clarke G.M., Curran J.;  
RT "Descriptions of three species of Eretmocerus Haldeman (Hymenoptera:  
RT Aphelinidae) parasitising Hemisia tabaci (Gennadius) (Hemiptera:  
RT Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:  
RT Aleyrodidae) in Australia based on morphological and molecular data.";  
RL Aust. J. Entomol. 0:0-0(2000).  
DR EMBL: AF275275; AAG25079.1; -.  
DR InterPro: IPR001505; COX2.  
DR InterPro: IPR002429; Cyt\_c\_ox\_2.  
DR Pfam: PF00116; COX2; 1.  
DR PRINTS: PR01166; CYCOXIDASEII.  
DR ProDom: PD000131; COX2; 1.  
KW Mitochondrion.  
FT NON\_TER 1  
FT NON\_TER 87  
SQ SEQUENCE 87 AA; 10387 MW; 43E205FB2E1C6FEC CRC64;

Query Match 100.0%; Score 26; DB 8; Length 87;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||

Db 81 DRVYI 85

RESULT 4  
Q9KG21 PRELIMINARY; PRT; 167 AA.  
ID Q9KG21  
AC Q9KG21;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE BH0294 PROTEIN.  
GN BH0294.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL: AP001508; BAB04013.1; -.  
KW Complete proteome.  
SQ SEQUENCE 167 AA; 19535 MW; 0C33F04D1A2E834D CRC64;

Query Match 100.0%; Score 26; DB 16; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||

Db 61 DRVYI 65

RESULT 5  
Q88184 PRELIMINARY; PRT; 173 AA.  
ID Q88184  
AC Q88184;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE RNA-DEPENDENT RNA POLYMERASE (FRAGMENT).  
OS San Miguel sea lion virus  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
OC Vesivirus.  
OX NCBI\_TaxID=111982;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SEROTYPE 5;  
RX MEDLINE=95287505; PubMed=7769708;  
RA Neill J.D., Meyer R.F., Seal B.S.;  
RT "Genetic relatedness of the caliciviruses: San Miguel sea lion and  
RT vesicular exanthema of swine viruses constitute a single genotype  
RT within the Caliciviridae.";  
RL J. Virol. 69:4484-4488(1995).  
DR EMBL: U18731; AAA82219.1; -.  
DR InterPro: IPR004004; Calici\_pol\_hel.  
DR PRINTS: PR00918; CALICIVIRUSN.  
KW RNA-directed RNA polymerase.  
FT NON\_TER 1  
FT NON\_TER 173  
SQ SEQUENCE 173 AA; 19532 MW; 1830C8461CC21F7F CRC64;

Query Match 100.0%; Score 26; DB 12; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 Db 50 DRVYI 54  
 |||||

RESULT 6  
 Q9HIS3 ID Q9HIS3 PRELIMINARY; PRT; 178 AA.  
 AC Q9HIS3  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE PROBABLE 50S RIBOSOMAL PROTEIN L6.  
 GN TAL255.  
 OS Thermoplasma acidophilum.  
 OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;  
 OC Thermoplasma  
 OX NCBI\_TaxID=2303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 1728;  
 RX MEDLINE=20479972; PubMed=11029001;  
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
 RA Newes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;  
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma  
 RT acidophilum";  
 RL Nature 407:508-513(2000).  
 DR EMBL; AL445067; CAC12379.1; -  
 DR InterPro; IPR000702; Ribosomal\_L6.  
 DR Pfam; PF00347; Ribosomal\_L6; 1.  
 DR ProDom; PD002236; Ribosomal\_L6; 1.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 178 AA; 19641 MW; 33B1312C268886A5 CRC64;

Query Match 100.0%; Score 26; DB 17; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 Db 134 DRVYI 138  
 |||||

RESULT 7  
 Q9W387 ID Q9W387 PRELIMINARY; PRT; 186 AA.  
 AC Q9W387  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE CG12664 PROTEIN.  
 GN LD14 OR CG12664.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.K., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003446; AAF46447.1; -  
 DR FlyBase; FBgn0030090; ldl4.  
 SQ SEQUENCE 186 AA; 20461 MW; D2B4ED097ACA6420 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 Db 110 DRVYI 114  
 |||||

RESULT 8  
 O28741 ID O28741 PRELIMINARY; PRT; 195 AA.  
 AC O28741  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
 DE CONSERVED HYPOTHETICAL PROTEIN.  
 GN AF1531.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;  
 OC Archaeoglobus  
 OX NCBI\_TaxID=2234;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475;  
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,  
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370(1997).  
DR EMBL: AF000997; AAB89717.1; -.  
DR TIGR: AF1531; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 195 AA; 23194 MW; C244F95420565E2C CRC64;

Query Match 100.0%; Score 26; DB 17; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
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|  
Db 68 DRVYI 72

RESULT 9  
Q973E6 PRELIMINARY; PRT; 199 AA.  
AC Q973E6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL PROTEIN ST0953.  
GN ST0953.  
OS Sulfolobus tokodaii.  
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
OX NCBI\_TaxID=111955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JCM 10545 / 7;  
RX PubMed=11572479;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sakine M., Baba S.-I., Akai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;  
RT "Complete genome sequence of an aerobic thermocacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";  
RL DNA Res. 8:123-140(2001).  
DR EMBL: AP000984; BAB65967.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 199 AA; 23401 MW; 7A42E708B18869D4 CRC64;

Query Match 100.0%; Score 26; DB 17; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
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Db 144 DRVYI 148

RESULT 10  
O66729 PRELIMINARY; PRT; 238 AA.  
AC O66729;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ABC TRANSPORTER.  
GN ABC7 OR AQ\_413.  
OS Aquifex aeolicus.  
OC Bacteria; Aquificales; Aquificaceae; Aquifex.  
OX NCBI\_TaxID=63363;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VF5;  
RX MEDLINE=98196666; PubMed=9537320;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Sneed M.A., Keller M., AuJay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";  
RL Nature 392:353-358(1998).  
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS).  
DR EMBL: AE000689; AAC06695.1; -.  
DR HSSP: Q58663; IG6H.  
DR InterPro: IPR003593; AAA.  
DR InterPro: IPR003439; ABC\_transportr.  
DR InterPro: IPR001687; ATP\_GTP\_A.  
DR Pfam: PF00005; ABC\_tran; 1.  
DR SMART: SM00382; AAA; 1.  
DR PROSITE: PS00211; ABC\_TRANSPORTER; 1.  
KW ATP-binding; Complete proteome; Transport.  
SQ SEQUENCE 238 AA; 26457 MW; 032A46CD90CEA8E5 CRC64;

Query Match 100.0%; Score 26; DB 16; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
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Db 202 DRVYI 206

RESULT 11  
Q95J13 PRELIMINARY; PRT; 245 AA.  
AC Q95J13;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN (FRAGMENT).  
GN REN.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=504, AND 505;  
RA Satta Y.;  
RT "Comparison of DNA and protein polymorphisms between humans and chimpanzees.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB062027; BAB55856.1; -.  
DR EMBL: AB062028; BAB55857.1; -.  
FT NON\_TER 245 245  
SQ SEQUENCE 245 AA; 26317 MW; E0092390B9803E0B CRC64;

Query Match 100.0%; Score 26; DB 6; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
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|  
Db 34 DRVYI 38

RESULT 12  
Q44326 PRELIMINARY; PRT; 248 AA.  
AC Q44326;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MOCC.  
GN MOCC.

```
OS Agrobacterium tumefaciens.
OC Plasmid Ti.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236046; PubMed=8655509;
RA Kim K.S., Farrand S.K.;
RT "Ti plasmid-encoded genes responsible for catabolism of the crown gall
RT opine mannopine by Agrobacterium tumefaciens are homologs of the T-
RT region genes responsible for synthesis of this opine by the plant
RT tumor.";
RL J. Bacteriol. 178:3275-3284(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
RA Farrand S.K.;
RT "Octopine-type Ti plasmid sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF242881; AAB07783.1; -.
DR HSSP; 070351; IE3S.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase; Plasmid.
SQ SEQUENCE 248 AA; 26810 MW; 10B69239CDEBB68D CRC64;

Query Match 100.0%; Score 26; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 DRVYI 5
Db 221 DRVYI 225

RESULT 13
O9C445 PRELIMINARY; PRT; 291 AA.
AC O9C445;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE PAXU.
GN PAXU.
OS Penicillium paxilli.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=70109;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21106005; PubMed=11169115;
RA Young C., McMillan L., Telfer E., Scott B.;
RT "Molecular cloning and genetic analysis of an indole-diterpene gene
RT cluster from Penicillium paxilli.";
RL Mol. Microbiol. 39:754-764(2001).
DR EMBL; AF279808; AAK11532.1; -.
SQ SEQUENCE 291 AA; 32954 MW; CFC35136FD40763E CRC64;

Query Match 100.0%; Score 26; DB 3; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 DRVYI 5
Db 16 DRVYI 20
```

```
RESULT 14
O9HBV1 PRELIMINARY; PRT; 291 AA.
AC O9HBV1;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE POPEYE PROTEIN 3.
GN POP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20341060; PubMed=10882522;
RA Andree B., Hillemann T., Kessler-Icekson G., Schmitt-John T.,
RA Jockusch H., Arnold H.H., Brand T.;
RT "Isolation and characterization of the novel popeye gene family
RT expressed in skeletal muscle and heart.";
RL Dev. Biol. 223:371-382(2000).
DR EMBL; AF204171; AAG23404.1; -.
SQ SEQUENCE 291 AA; 33810 MW; 49B6EF5DBC02DDC2 CRC64;

Query Match 100.0%; Score 26; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 DRVYI 5
Db 248 DRVYI 252

RESULT 15
O9ES81 PRELIMINARY; PRT; 291 AA.
AC O9ES81;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE POPEYE PROTEIN 3.
GN POP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20341060; PubMed=10882522;
RA Andree B., Hillemann T., Kessler-Icekson G., Schmitt-John T.,
RA Jockusch H., Arnold H.H., Brand T.;
RT "Isolation and characterization of the novel popeye gene family
RT expressed in skeletal muscle and heart.";
RL Dev. Biol. 223:371-382(2000).
DR EMBL; AF204176; AAG23409.1; -.
DR MGD; MGI:1930153; Pop3.
SQ SEQUENCE 291 AA; 33612 MW; 8AC6BFE107AEEL2 CRC64;

Query Match 100.0%; Score 26; DB 11; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 DRVYI 5
Db 248 DRVYI 252
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Search completed: July 1, 2002, 07:45:14  
Job time: 410 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 seconds  
(without alignments)  
2.807 Million cell updates/sec

Title: US-09-723-197-10  
Perfect score: 22  
Sequence: 1 DRVY 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	4	17	AA195671
2	22	100.0	4	19	AA195671
3	22	100.0	4	19	AA195671
4	22	100.0	4	19	AA195671
5	22	100.0	4	20	AA195671
6	22	100.0	4	20	AA195671
7	22	100.0	4	20	AA195671
8	22	100.0	4	20	AA195671
9	22	100.0	4	20	AA195671
10	22	100.0	4	20	AA195671
11	22	100.0	4	20	AA195671

12	22	100.0	4	20	AA15314	Angiotensin II (AI
13	22	100.0	4	21	AA15314	Angiotensin II ana
14	22	100.0	4	21	AA15314	Angiotensin II ana
15	22	100.0	4	21	AA15314	Peptide comprising
16	22	100.0	4	21	AA15314	Angiotensin II (AI
17	22	100.0	4	21	AA15314	Angiotensin peptid
18	22	100.0	4	22	AA15314	Human angiotensin
19	22	100.0	4	22	AA15314	Human angiotensin
20	22	100.0	4	22	AA15314	Human angiotensin
21	22	100.0	4	22	AA15314	Angiotensin peptid
22	22	100.0	4	22	AA15314	Angiotensin II fra
23	22	100.0	5	19	AA15314	Angiotensin II pep
24	22	100.0	5	19	AA15314	Angiotensin II ana
25	22	100.0	5	19	AA15314	Peptide AII(1-5) u
26	22	100.0	5	20	AA15314	Angiotensin analog
27	22	100.0	5	20	AA15314	Angiotensin II ana
28	22	100.0	5	20	AA15314	Amino acid sequenc
29	22	100.0	5	20	AA15314	Amino acid sequenc
30	22	100.0	5	20	AA15314	Angiotensin II ana
31	22	100.0	5	20	AA15314	Angiotensin II (AI
32	22	100.0	5	20	AA15314	Angiotensin II (AI
33	22	100.0	5	20	AA15314	Angiotensin II (AI
34	22	100.0	5	21	AA15314	Angiotensin II ana
35	22	100.0	5	21	AA15314	Angiotensin II ana
36	22	100.0	5	21	AA15314	Amino acid sequenc
37	22	100.0	5	21	AA15314	Peptide comprising
38	22	100.0	5	21	AA15314	Angiotensin II (AI
39	22	100.0	5	21	AA15314	Angiotensin peptid
40	22	100.0	5	22	AA15314	Angiotensin peptid
41	22	100.0	5	22	AA15314	Human angiotensin
42	22	100.0	5	22	AA15314	Human angiotensin
43	22	100.0	5	22	AA15314	C-terminally trunc
44	22	100.0	6	17	AA15314	Angiotensin II fra
45	22	100.0	6	19	AA15314	Angiotensin II ana

ALIGNMENTS

RESULT 1	
AA195671	AA195671 standard; peptide; 4 AA.
XX	
AC	AA195671;
XX	
DT	09-JAN-1997 (first entry)
XX	
DE	Angiotensin II fragment AII(1-4).
XX	
KW	Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW	angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW	ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX	
OS	Synthetic.
XX	
PN	WO9614858-A1.
XX	
PD	23-MAY-1996.
XX	
PF	14-NOV-1995; 95WO-US14764.
XX	
PR	06-JUN-1995; 95US-0465775.
XX	
PA	14-NOV-1994; 94US-0337781.
XX	
PI	(UYSC-) UNIV SOUTHERN CALIFORNIA.
XX	
DR	Dizerega GS, Rodgers K;
XX	
PT	WPI; 1996-259561/26.
PT	Accelerating wound healing by application of angiotensin II
PT	fragments - are effective at very low concn. and do not cause
PT	hypertension

XX Disclosure; Page 4; 46pp; English.  
 XX AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see  
 CC AAR95662) is an octapeptide present in humans and other species. AT2 is  
 CC one of the most potent vasoconstrictors known, causing constriction of  
 CC the arterioles. The formation of angiotensin is initiated by the action  
 CC of renin on angiotensinogen. The substance formed is a decapeptide  
 CC called angiotensin I which is converted by the enzyme angiotensinase (by  
 CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release  
 CC of extracellular matrices involved in wound repair. These fragments can  
 CC be used in a compound for accelerating wound healing. The compounds are  
 CC administered as matricial or micellar solutions, formulated with a  
 CC carrier or diluent, alternatively the compound is applied in conjuncture  
 CC with a wound dressing. The carrier used in the composition is  
 CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly  
 CC glycols. By using fragments of this sequence (or analogues of it),  
 CC growth as well as healing of tissues is improved, such as in cases of  
 CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or  
 CC intraperitoneal surgical wounds. The compounds containing the AT2  
 CC fragments are less hypertensive than full length AT2, and are also  
 CC effective at much lower (nanomolar) concentrations than full length AT2.  
 XX Sequence 4 AA;

Query Match 100.0%; Score 22; DB 17; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
 Db 1 drvy 4

RESULT 2  
 AAW64737  
 ID AAW64737 standard; peptide: 4 AA.  
 XX AAW64737;  
 XX  
 XX 02-NOV-1998 (first entry)  
 XX  
 XX Angiotensin II peptide #9.  
 XX  
 XX Proliferation; mesenchymal stem cell; lineage-specific cell;  
 KW haematopoietic; cell culture; transplantation; treatment; malignant;  
 KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9832457-A2.  
 XX  
 XX 30-JUL-1998.  
 XX  
 XX 26-JAN-1998; 98WO-US01552.  
 XX  
 XX 23-JAN-1998; 98US-0066593.  
 PR 28-JAN-1997; 97US-0036507.  
 PR 08-MAY-1997; 97US-0046859.  
 PR 28-OCT-1997; 97US-0063684.  
 PR 31-OCT-1997; 97US-0063910.  
 PR 18-NOV-1997; 97US-0065612.  
 PR 26-NOV-1997; 97US-0066593.  
 XX  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PA  
 XX Dizerega G, Rodgers KE;  
 PI  
 XX WPI; 1998-437044/37.  
 DR  
 XX Promoting haematopoietic and mesenchymal cell proliferation and

PT differentiation - by contacting the cells with angiotensinogen,  
 XX angiotensin I or II, or analogues or fragments of these  
 XX Claim 7; Page 14; 114pp; English.  
 PS  
 XX AAW64728-W64763 are peptides used in a novel method for accelerating the  
 CC proliferation of mesenchymal stem cells (MSCs), haematopoietic  
 CC lineage-specific cells or mesenchymal lineage-specific cells. The method  
 CC involves contacting the cells with an active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R1-R8 in  
 CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together  
 CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,  
 CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane  
 CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoser or  
 CC azatyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or  
 CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are  
 CC not defined in the specification, the peptide bond between Ra and Rb is  
 CC labile to aminopeptidase A cleavage excluding sequences including R4 as a  
 CC terminal Tyr group. A second active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R2-R8 in  
 CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,  
 CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also  
 CC described, the inventions are particularly useful in cell culture  
 CC mediums. These cells may be used in transplantation techniques for  
 CC treatment of malignant or inherited diseases. The formulae represent  
 CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),  
 CC or AII AT2 type 2 receptor agonists.  
 XX Sequence 4 AA;

Query Match 100.0%; Score 22; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
 Db 1 drvy 4

RESULT 3  
 AAW65606  
 ID AAW65606 standard; peptide: 4 AA.  
 XX AAW65606;  
 XX  
 XX 09-NOV-1998 (first entry)  
 XX  
 XX Angiotensin II analogue, AII(1-4).  
 XX  
 XX angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;  
 KW wound healing.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9826795-A1.  
 XX  
 XX 25-JUN-1998.  
 XX  
 XX 16-DEC-1997; 97WO-US23461.  
 XX  
 XX 15-DEC-1997; 97US-0990664.  
 PR 16-DEC-1996; 96US-0028310.  
 XX  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PA  
 XX Dizerega GS, Rodgers KE;  
 PI  
 XX WPI; 1998-362518/31.  
 DR  
 XX Promoting incorporation of skin graft onto underlying tissue -  
 PT comprises pre-treating graft with angiotensin II, or analogue or



PT peptide fragment

PS Disclosure; Page 6; 82pp; English.

XX The invention relates to the use of angiotensin II (AII), AII analogues, CC AII fragments and AII fragment analogues for promoting incorporation of a CC skin graft into underlying tissue of a mammal. The peptides are effective CC in accelerating the growth or healing of skin grafts and in accelerating CC re-epithelialisation and tissue repair, even at very low concentrations. CC They can significantly accelerate the rate of healing at nanomolar levels CC in vivo. AII accelerates wound repair by increased neovascularisation, CC growth factor release, re-epithelialisation, extracellular matrix production CC and increased flow of blood and nutrients to the injured tissue. Use of CC the above peptides other than AII itself (an extremely potent vaso- CC constrictor) may avoid the side-effects of AII, such as increase in blood CC pressure and thirst. The present sequence represents an angiotensin CC II fragment.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 19; Length 4;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

Db 1 | | | |

1 drvY 4

RESULT 4

AAW71119

ID AAW71119 standard; peptide; 4 AA.

AC AAW71119;

XX 27-OCT-1998 (first entry)

DT Peptide AII(1-4) used to accelerate thermal wound healing.

XX Angiotensin; AII; acceleration; thermal wound healing; human;

XX growth factor release; neovascularisation; re-epithelialisation;

KW extracellular matrix production.

KW Synthetic.

OS WO9833813-A2.

XX 06-AUG-1998.

PD 04-FEB-1998; 98WO-US02049.

XX 04-FEB-1997; 97US-0037166.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

PA Dizerega G, Rodgers KE;

PI WPI; 1998-437391/37.

XX Methods for accelerating thermal wound healing in humans - using

XX angiotensinogen II and AII analogues

PT Claim 3; Page 9; 58pp; English.

PS AAW71110-27 represent peptide used in the method of the invention. The

XX specification describes a method of accelerating thermal wound healing

XX in humans. The method comprises applying to the thermally injured tissue

XX an amount of at least one active agent which comprises the peptides

XX AAW7115-27. The method can be used to promote the healing of thermal

XX wounds by accelerating growth factor release, neovascularisation,

XX re-epithelialisation and extracellular matrix production. The sequences

XX are analogues of the angiotensin or angiotensinogen family of proteins.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 19; Length 4;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

Db 1 | | | |

1 drvY 4

RESULT 5

AAAY49595

ID AAY49595 standard; peptide; 4 AA.

XX AC AAY49595;

XX 13-JAN-2000 (first entry)

DT Angiotensin analogue peptide SEQ ID NO:10.

XX Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;

XX receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.

KW Synthetic.

OS WO9952540-A1.

XX 21-OCT-1999.

PD 07-APR-1999; 99WO-US07654.

XX 09-APR-1998; 98US-0081262.

XX 12-JUN-1998; 98US-0089024.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

PA Rodgers KE, Dizerega G;

XX WPI; 1999-620285/53.

XX Treating or preventing infections in mammals using peptides derived

XX from angiotensin or angiotensin receptor agonists

XX Claim 2; Page 10; 91pp; English.

XX The present invention describes a method for treating or preventing

XX infections in mammals by administering peptides (A) that are fragments

XX or analogues (or their fragments) of angiotensinogen, angiotensins I or

XX II, or angiotensin II AT<sub>2</sub>-type receptor agonists. (A) contain at least

XX 3 consecutive amino acids (aa) from the sequence (S1):

XX R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;

XX X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane

XX carboxylic acid), Ala, dimethylglycine, pro, betaine, Glu(NH<sub>2</sub>), Gly,

XX Asp(NH<sub>2</sub>) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,

XX sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,

XX Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr

XX (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;

XX R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;

XX R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =

XX sequences having R4 as a terminal Tyr residue are excluded. The method

XX is particularly used in cases of bacterial infection (e.g. septic shock,

XX peritonitis, bacteraemia or endotoxaemia) but also against viral and

XX parasitic infections. AAY49586 to AAY49623 represent specifically

XX claimed examples of (A).

XX SQ Sequence 4 AA;

Query Match

Best Local Similarity 100.0%; Score 22; DB 20; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
| | | |  
Db 1 drvy 4

## RESULT 6

AAV33910  
ID AAY33910 standard; peptide: 4 AA.

XX AC AAY33910;

XX XX 29-NOV-1999 (first entry)

XX XX Angiotensin II analogue AII(1-4).

XX KW embryonic stem cell; ES; angiotensin; totipotent cell;  
XX KW gene therapy; replacement therapy; angiotensin II; AII;  
XX KW analogue.

XX OS Homo sapiens.

XX XX WO9942122-A1.

XX XX 26-AUG-1999.

XX XX 16-FEB-1999; 99WO-US03243.

XX XX 19-FEB-1998; 98US-0075179.

XX XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX XX Dizerega G, Rodgers KE;

XX XX WPI; 1999-527419/44.

XX PT Promoting embryonal cell proliferation, using angiotensinogen and  
XX PT angiotensin peptides, analogs or fragments

XX PS Claim 2; Page 8; 76pp; English.

XX CC This is the amino acid sequence of the Angiotensin II analogue,  
XX CC AII(1-4). The formation of Angiotensin II (AII) is initiated by the  
XX CC action of renin on the plasma substrate angiotensinogen.  
XX CC This results in Angiotensin I (AI) which then converted to AII by the  
XX CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
XX CC residues from AI (AAY42372).  
XX CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and  
XX CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,  
XX CC or AII A2 type 2 receptor agonists can rapidly provide a large  
XX CC population of ESCs (Embryonic Stem Cell) for use in replacement therapy.  
XX CC Similarly, methods that increase in vivo proliferation of ESCs will  
XX CC enhance the utility of replacement therapy by rapidly increasing local  
XX CC concentration of the stem cells and their progeny at the site of  
XX CC therapy. The method also increases the potential utility of ESCs as  
XX CC vehicles for gene therapy in certain disorders by more efficiently  
XX CC providing a large number of such cells for transfection, and also by  
XX CC providing a more efficient means to rapidly expand transfectd ESCs.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
| | | |  
Db 1 drvy 4

## RESULT 7

AAV30548

XX ID AAY30548 standard; peptide: 4 AA.

XX AC AAY30548;

XX XX 18-NOV-1999 (first entry)

XX XX Amino acid sequence of angiotensin II fragment AII1-4.

XX DE Angiotensin; analogue; tissue equivalent; cell proliferation.

XX XX Synthetic.

XX XX WO9946285-A2.

XX XX 16-SEP-1999.

XX PF 11-MAR-1999; 99WO-US05261.

XX PR 11-MAR-1998; 98US-0077499.

XX PR 12-JUN-1998; 98US-0089064.

XX XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX XX Rodgers KE, Dizerega G;

XX XX WPI; 1999-551360/46.

XX PT An improved method for producing a tissue equivalent with angiotensin I  
XX PT and II derived active agents -

XX PS Claim 2; Page 57; 83pp; English.

XX CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII  
XX CC fragments and AII analogs. The peptides are used in the method  
XX CC of the invention. The specification describes an improved method  
XX CC for producing a tissue equivalent. The method comprises contacting  
XX CC the tissue equivalent with angiotensin I and II derived active  
XX CC agents. The methods are used for production and culture of tissue  
XX CC equivalents (three-dimensional cell and tissue culture systems),  
XX CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,  
XX CC vascular graft, cartilage, ligament, collagen lattice, liver and  
XX CC kidney tissue equivalents. The methods and tissue culture systems  
XX CC are used for the long-term proliferation of cells and tissues  
XX CC in an in vitro environment that more closely approximates that found  
XX CC in vivo.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4

| | | |

Db 1 drvy 4

## RESULT 8

AAV30592  
ID AAY30592 standard; peptide: 4 AA.

XX AC AAY30592;

XX XX 18-NOV-1999 (first entry)

XX XX Amino acid sequence of an angiotensin II (AII) fragment AII1-4.

XX KW Angiotensin; analogue; radiation mitigation; tissue damage;

XX KW radiation therapy; bone marrow transplantation; cancer therapy;

XX KW megakaryocyte production; platelet production; cancer therapy;

XX KW gene therapy; hematopoietic disorder.

XX OS Synthetic.  
 XX PN WO9945945-A1.  
 XX PD 16-SEP-1999.  
 XX PF 08-MAR-1999; 99WO-US05194.  
 XX PR 10-MAR-1998; 98US-0077382.  
 XX PR 09-APR-1998; 98US-0081262.  
 XX PR 30-APR-1998; 98US-0083670.  
 XX PR 19-JUN-1998; 98US-0090096.  
 XX PR 22-JUN-1998; 98US-0090216.  
 XX PR 11-SEP-1998; 98US-0099957.  
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PA (RODG/) RODGERS K E.  
 XX PA (DIZE/) DIZEREGA G.  
 XX PI Rodgers KE, Dizerega G;  
 XX PF WPI; 1999-551209/46.  
 XX PR Use of angiotensin and angiotensin type peptides, for mitigating  
 XX PT radiation induced tissue damage, improving bone marrow transplantation  
 XX PT and promoting megakaryocyte and platelet production -  
 XX PS Claim 2; Page 90; 116pp; English.  
 XX CC AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII  
 CC fragments and AII analogues. The peptides are used in the method  
 CC of the invention. The specification describes a method for mitigating  
 CC radiation induced tissue damage, improving the effectiveness of  
 CC radiation therapy, to support bone marrow transplantation, and  
 CC promoting megakaryocyte production and mobilization and platelet  
 CC production. The method comprises administration of the present peptides.  
 CC The methods can be used to mitigate radiation induced tissue damage, to  
 CC improve the effectiveness of radiation therapy, to support bone marrow  
 CC transplantation, and to promote megakaryocyte production and  
 CC mobilization and platelet production. They are used particularly in  
 CC cancer therapy. They can also be used to provide megakaryocytes as  
 CC vehicles for gene therapy in hematopoietic disorders, by providing a  
 CC more efficient means to rapidly expand transduced megakaryocytes.  
 XX SQ Sequence 4 AA;  
 Query Match 100.0%; Score 22; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVY 4  
 Db ||||  
 1 drvy 4  
 RESULT 9  
 AAY32723  
 ID AAY32723 standard; peptide; 4 AA.  
 XX AC AAY32723;  
 XX AC  
 XX DT 09-NOV-1999 (first entry)  
 XX DE Angiotensin II analogue AII(1-4).  
 XX KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;  
 KW chemotaxis; growth factor; liver regeneration; cirrhosis;  
 KW hepatocarcinoma; hepatectomy; transplantation.  
 XX OS Synthetic.  
 OS Homo sapiens.

XX WO9939743-A2.  
 XX PN 12-AUG-1999.  
 XX PD 08-FEB-1999; 99WO-US02618.  
 XX PF 13-NOV-1998; 98US-0108412.  
 XX PR 09-FEB-1998; 98US-0074104.  
 XX PA (DIZE/) DIZEREGA G.  
 XX PA (RODG/) RODGERS K E.  
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX PI Dizerega G, Rodgers KE;  
 XX PF WPI; 1999-508461/42.  
 XX DR Hepatic cell proliferation with angiotensin I and II derived active  
 XX PT agents, useful for regeneration of liver after resection  
 XX PS Claim 2; Page 9; 66pp; English.  
 XX CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The  
 CC peptides are derived from the AII peptide (AAY32750). AII increases  
 CC mitogenesis and chemotaxis in cultured cells, and also increases the  
 CC release of growth factors and extracellular matrices. AII has also been  
 CC shown to increase the proliferation of certain cell types. The AII  
 CC analogue peptides can be used as the active agent in a method for  
 CC promoting hepatic cell proliferation and differentiation. The method  
 CC involves contacting the hepatic cells with an amount effective enough to  
 CC promote proliferation of any of the peptides. This method is useful in  
 CC liver regeneration following resection of hepatocarcinomas, hepatitis  
 CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic  
 CC failure, hepatocyte transplantation, liver transplantation and other  
 CC hepatic disorders where rapid regeneration of the liver is desirable. The  
 CC methods are also useful in rapidly providing a large population of  
 CC hepatic cells for use in cell therapy and for providing a large  
 CC population of transduced hepatic cells for use in gene therapy.  
 XX SQ Sequence 4 AA;  
 Query Match 100.0%; Score 22; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVY 4  
 Db ||||  
 1 drvy 4  
 RESULT 10  
 AAY33777  
 ID AAY33777 standard; peptide; 4 AA.  
 XX AC AAY33777;  
 XX AC  
 XX DT 09-NOV-1999 (first entry)  
 XX DE Angiotensin II (AII) octapeptide fragment AII(1-4).  
 XX KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;  
 KW neuronal cell proliferation; differentiation; Alzheimer's disease;  
 KW Parkinson's disease; neuron replacement therapy.  
 XX OS Homo sapiens.  
 XX PN WO9942123-A1.  
 XX PD 26-AUG-1999.  
 XX PF 19-FEB-1999; 99WO-US03772.

XX 19-FEB-1998; 98US-0075232.  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 XX WPI; 1999-527420/44.  
 XX Promoting neuronal cell proliferation and differentiation  
 XX Claim 2; Page 10; 62pp; English.  
 XX Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The application of angiotensin to wound tissue significantly increases the rate of wound healing. AII is known to increase mitogenesis and chemotaxis in cultured cells, and also increases their release of growth factors and extracellular matrices, implicating it in cell growth and differentiation. AT2 receptors are receptors for AII and are thought to be involved in the mediation of the cell differentiation effects of AII. Peptides AAY33768-Y33802 are used in a method for promoting neuronal cell proliferation or differentiation. This method is useful in the treatment of Alzheimer's and Parkinson's diseases by neuron replacement therapy.  
 XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 22; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVY 4  
 Db 1 drvy 4  
 ||||

RESULT 11  
 AAY15354  
 ID AAY15354 standard; peptide; 4 AA.  
 XX AAY15354;  
 AC  
 DT 09-NOV-1999 (first entry)  
 XX  
 DE Angiotensin II (AII) analogue, AII(1-4).  
 XX burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;  
 KW AII; analogue; chronic renal failure; cancer; bone marrow.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9940106-A2.  
 PN 12-AUG-1999.  
 XX  
 PD 08-FEB-1999; 99WO-US02648.  
 PF  
 XX 09-DEC-1998; 98US-0111535.  
 PR 09-FEB-1998; 98US-0074106.  
 XX  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 XX WPI; 1999-508486/42.  
 XX Promoting erythropoiesis with angiotensin I and II derived active agents, useful for treatment of, e.g. congenital or acquired aplastic or hypoplastic anemia  
 XX

PS Claim 2; Page 10; 76pp; English.  
 XX This sequence is an angiotensin II (AII) analogue. Similar sequences also based on the AII peptide have been tested against each other, AII and a negative control. These active agents have been shown to affect the levels of BFU-E (burst forming units-erythroid) in culture. The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380) augment erythropoiesis by potentiating erythropoietin-induced differentiation. Increasing the rate of erythropoiesis improves clinical benefits for the treatment of congenital or acquired aplastic or hypoplastic anemia associated with chronic renal failure, end-stage renal disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy, bone marrow transplantation and chronic diseases.  
 XX The active agents permit the use of smaller doses of erythropoietin therefore decreasing treatment costs.  
 XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 22; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVY 4  
 Db 1 drvy 4  
 ||||

RESULT 12  
 AAY15314  
 ID AAY15314 standard; peptide; 4 AA.  
 XX AAY15314;  
 AC  
 DT 09-NOV-1999 (first entry)  
 XX  
 DE Angiotensin II (AII) analogue, AII(1-4).  
 XX angiotensin; angiotensin II; AII; wound healing; scarring;  
 KW tissue repair; agonist; analogue.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9940107-A2.  
 PN 12-AUG-1999.  
 XX  
 PD 08-FEB-1999; 99WO-US02725.  
 PF  
 XX 09-FEB-1998; 98US-0074105.  
 PR  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 XX WPI; 1999-508487/42.  
 XX Epithelial stem cell and keratinocyte proliferation with angiotensin I and II derived active agents, useful for treatment of skin wounds  
 XX Claim 2; Page 10; 70pp; English.  
 XX This is the amino acid sequence of an Angiotensin II analogue. This and other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337) can be used to promote the proliferation of epithelial stem cells and keratinocytes leading to a more rapid and efficient cellular response to stratified epithelial injury. The angiotensin analogues are derived from an octapeptide present in humans and other species which has the sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as angiotensin II (AII). This is formed by the action of renin on the plasma substrate angiotensinogen, the product of this reaction is a decapeptide called angiotensin I (AI) which is converted to AII by the

CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
CC residues from AI (AAY15339).

XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
|  
|  
|  
|  
Db 1 drvy 4

## RESULT 13

AAB27410  
ID AAB27410 standard; Peptide: 4 AA.

XX AC AAB27410;

XX DT 23-JAN-2001 (first entry)

XX DE Angiotensin II analog AII(1-4).

XX KW Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;  
XX KW cardiomyopathies; inflammation; infection; sepsis; ischemia;  
XX KW heart valve disease; myocarditis; angiotensin.

XX OS Synthetic.

XX PN WO200053211-A2.

XX PD 14-SEP-2000.

XX PF 09-MAR-2000; 2000WO-US06198.

XX PR 09-MAR-1999; 99US-0123678.

XX PR 31-AUG-1999; 99US-0151874.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers K, Dizerega G;

XX DR WPI; 2000-611400/58.

XX PT Promoting myocyte proliferation and myocardial tissue repair by  
PT contacting myocytes with angiotensinogen or angiotensin I or II, useful  
PT for treating heart attacks, cardiomyopathies, inflammation and  
PT infection.

XX PS Claim 2; Page 10; 55pp; English.

XX CC The present invention relates to a method of promoting myocyte  
CC proliferation or differentiation by contacting myocytes with an active  
CC agent containing angiotensinogen, angiotensin I and II (AI, AII), and  
CC angiotensin analogs. The present sequence is an angiotensin II analog  
CC of the invention. The active agents of the invention may be useful for  
CC promoting myocardial tissue repair following myocardial injury and for  
CC treating heart failure in a mammal. Administration to accelerate in  
CC vivo myocyte proliferation and/or to treat myocardial injuries can be  
CC used to treat cardiomyopathies, inflammation, infection, sepsis,  
CC ischemia, heart valve disease, myocarditis, inflammation, myocardial  
CC ischemia and infarction and for improving cardiac output by increasing  
CC stroke volume.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 21; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
|  
|  
|  
|  
Db 1 drvy 4

## RESULT 14

AAB28108  
ID AAB28108 standard; Peptide: 4 AA.

XX AC AAB28108;

XX DT 26-JAN-2001 (first entry)

XX DE Angiotensin II analogue SEQ ID NO: 10.

XX KW Wound; scar formation; healing; adhesion formation; AII;  
XX KW angiotensin II analogue; scar treatment.

XX OS Synthetic.

XX PN WO200056345-A2.

XX PD 28-SEP-2000.

XX PF 22-MAR-2000; 2000WO-US07669.

XX PR 23-MAR-1999; 99US-0125707.

XX PR 16-JUN-1999; 99US-0139541.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers K, Dizerega G;

XX DR WPI; 2000-587607/55.

XX PT Limiting scar or adhesion formation comprises administering at least  
PT one active agent comprising a peptide.

XX PS Claim 2; Page 10; 54pp; English.

XX CC The present invention is concerned with peptide analogues of angiotensin  
CC II (AII) which can be used to limit scar and adhesion formation. The  
CC application of AII to wound tissue results in a rapid increase in the  
CC rate of wound healing and causes the proliferation of certain cells, such  
CC as epithelial cells and keratinocytes. Analogues of the protein have been  
CC shown to reduce scar formation, and can be used not only to limit new  
CC scar formation but also to therapeutically treat existing scars. The  
CC wound types include lacerations, burns, punctures, trauma, ulcers,  
CC periodontal conditions, laparotomy and incisional wounds, revision of  
CC hypertrophic scars, genetic hypertrophic scars, keloid scars,  
CC contractures after burns and cosmetic surgical procedures.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 21; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
|  
|  
|  
|  
Db 1 drvy 4

## RESULT 15

AAY84133  
ID AAY84133 standard; peptide; 4 AA.

XX AC AAY84133;

XX DT 03-JUL-2000 (first entry)

XX DE Peptide comprising amino acids 1-4 of angiotensin II.

XX Angiotensin III; angiotensinogen; angiotensin I; angiotensin II;  
 KW analogue; blood flow; ischemic tissue; angiogenesis; cardiac remodelling;  
 KW congestive heart disease; ischemic myocardial infarction;  
 KW embryonic development; wound healing; chronic inflammatory disease.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200009144-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 XX 12-AUG-1999; 99WO-US18374.  
 XX  
 PR 13-AUG-1998; 98US-0096414.  
 PR 18-SEP-1998; 98US-0101024.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Rodgers K, Dizerega G;  
 XX  
 DR WPI; 2000-237409/20.  
 XX  
 PT Increasing blood flow to ischemic tissue for minimizing cardiac  
 PT remodelling and development of congestive heart failure involves  
 PT administration of an active agent  
 XX  
 PS Claim 2; Page 42; 56pp; English.  
 XX  
 CC The present sequence represents an angiotensin II fragment. The  
 CC specification also describes peptides derived from angiotensinogen,  
 CC angiotensin I, angiotensin II, angiotensin III, and their analogues.  
 CC The peptides are used for increasing blood flow to ischemic tissue.  
 CC The peptides are angiogenesis stimulators. The peptides are useful for  
 CC increasing blood flow to ischemic tissue by stimulating angiogenesis,  
 CC and minimizing cardiac remodelling and development of congestive heart  
 CC disease following a ischemic myocardial infarction. The stimulation of  
 CC angiogenesis is also useful for embryonic development, wound healing  
 CC and treating chronic inflammatory disease.  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
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 Db 1 drvy 4

Search completed: July 1, 2002, 07:41:55  
 Job time: 347 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:01 ; Search time 59.1 Seconds  
(without alignments)  
1.653 Million cell updates/sec

Title: US-09-723-197-10  
Sequence: 1 DRVY 4

Scoring table: BLOSUM62  
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Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	4	2	US-08-465-775-10
2	22	100.0	4	3	US-09-208-337-10
3	22	100.0	4	3	US-08-990-664-11
4	22	100.0	4	4	US-09-373-962-10
5	22	100.0	4	4	US-09-245-680-10
6	22	100.0	4	4	US-09-198-806C-10
7	22	100.0	4	4	US-09-352-191-10
8	22	100.0	4	4	US-09-012-400-10
9	22	100.0	5	2	US-08-465-775-9
10	22	100.0	5	3	US-09-208-337-9
11	22	100.0	5	3	US-08-990-664-10
12	22	100.0	5	4	US-09-373-962-9
13	22	100.0	5	4	US-09-245-680-9
14	22	100.0	5	4	US-09-198-806C-9
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16	22	100.0	5	4	US-09-012-400-9
17	22	100.0	6	2	US-08-465-775-8
18	22	100.0	6	3	US-09-208-337-8
19	22	100.0	6	3	US-08-990-664-9
20	22	100.0	6	4	US-09-373-962-8
21	22	100.0	6	4	US-09-245-680-8
22	22	100.0	6	4	US-09-198-806C-8
23	22	100.0	6	4	US-09-352-191-8
24	22	100.0	6	4	US-09-012-400-8
25	22	100.0	7	2	US-08-465-775-4
26	22	100.0	7	2	US-09-047-594-1
27	22	100.0	7	3	US-09-208-337-4

28	22	100.0	7	3	US-08-990-664-5	Sequence 5, Appli
29	22	100.0	7	4	US-09-373-962-4	Sequence 4, Appli
30	22	100.0	7	4	US-09-245-680-4	Sequence 4, Appli
31	22	100.0	7	4	US-09-198-806C-4	Sequence 4, Appli
32	22	100.0	7	4	US-09-352-191-4	Sequence 4, Appli
33	22	100.0	7	4	US-09-012-400-4	Sequence 4, Appli
34	22	100.0	7	6	5451571-4	Patent No. 5451571
35	22	100.0	8	1	US-07-858-842-2	Sequence 2, Appli
36	22	100.0	8	1	US-08-021-839A-3	Sequence 3, Appli
37	22	100.0	8	1	US-08-184-935-2	Sequence 2, Appli
38	22	100.0	8	1	US-08-212-433A-29	Sequence 29, Appli
39	22	100.0	8	1	US-08-185-448-8	Sequence 8, Appli
40	22	100.0	8	1	US-07-776-272-1	Sequence 1, Appli
41	22	100.0	8	1	US-08-428-488-21	Sequence 21, Appli
42	22	100.0	8	1	US-08-337-781-1	Sequence 1, Appli
43	22	100.0	8	1	US-08-240-711-20	Sequence 20, Appli
44	22	100.0	8	1	US-08-594-117-1	Sequence 1, Appli
45	22	100.0	8	1	US-08-594-117-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-465-775-10  
; Sequence 10, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOGENIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-775-10

Query Match 100.0%; Score 22; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVY 4

Db 1 DRVY 4

RESULT 2  
US-09-208-337-10  
; Sequence 10, Application US/09208337  
; Patent No. 6096709  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: Gere, dizerega  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,337  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,775  
; FILING DATE: 06-JUN-1995  
; APPLICATION NUMBER: 08/337,781  
; FILING DATE: 14-NOV-1994  
; APPLICATION NUMBER: 08/126,368  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC010.001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 949-760-0404  
; TELEFAX: 949-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-09-208-337-10  
  
Query Match 100.0%; Score 22; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVY 4  
Db 1 DRVY 4  
  
RESULT 3  
US-08-990-664-11  
; Sequence 11, Application US/08990664  
; Patent No. 6110895  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
; TITLE OF INVENTION: IN SKIN GRAFTS  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/990,664  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/028,310  
; FILING DATE: 16-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC012.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-760-0404  
; TELEFAX: 714-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-990-664-11  
  
Query Match 100.0%; Score 22; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVY 4  
Db 1 DRVY 4  
  
RESULT 4  
US-09-373-962-10  
; Sequence 10, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)  
US-09-373-962-10  
  
Query Match 100.0%; Score 22; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVY 4  
Db 1 DRVY 4



```

; TITLE OF INVENTION: Growth and Repair
; FILE REFERENCE: 98365B
; CURRENT APPLICATION NUMBER: US/09/352,191
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-352-191-10

Query Match      100.0%; Score 22; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4
   ||||
Db 1 DRVY 4

RESULT 8
US-09-012-400-10
; Sequence 10, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
; TITLE OF INVENTION: Proliferation and Differentiation
; FILE REFERENCE: 97,017-G
; CURRENT APPLICATION NUMBER: US/09/012,400D
; CURRENT FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)
US-09-012-400-10

Query Match      100.0%; Score 22; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4
   ||||
Db 1 DRVY 4

RESULT 9
US-08-465-775-9
; Sequence 9, Application US/08465775
; Patent No. 5955430
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: dizerega, Gere S.
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Robbins, Berliner & Carson
; STREET: 201 No. 5955430th Figueroa Street #500
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90012

```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/465,775  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-360  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 9:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-775-9

Query Match 100.0%; Score 22; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
Db 1 DRVY 4

RESULT 10  
US-09-208-337-9  
Sequence 9, Application US/09208337  
Patent No. 6096709  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: Gere, diZerega  
TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/208,337  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,775  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: 08/337,781  
FILING DATE: 14-NOV-1994  
APPLICATION NUMBER: 08/126,368  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E.  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: USC010.001CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 949-760-0404

TELEFAX: 949-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-208-337-9

Query Match 100.0%; Score 22; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
Db 1 DRVY 4

RESULT 11  
US-08-990-664-10  
Sequence 10, Application US/08990664  
Patent No. 6110895  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: diZerega, Gere  
TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
TITLE OF INVENTION: IN SKIN GRAFTS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/990,664  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,310  
FILING DATE: 16-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E.  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: USC012.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-990-664-10

Query Match 100.0%; Score 22; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

Db 1 DRVY 4  
||||

## RESULT 12

US-09-373-962-9  
; Sequence 9, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373.962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-373-962-9

Query Match 100.0%; Score 22; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
||||  
Db 1 DRVY 4

## RESULT 13

US-09-245-680-9  
; Sequence 9, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245.680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-245-680-9

Query Match 100.0%; Score 22; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
||||  
Db 1 DRVY 4

## RESULT 14

US-09-198-806C-9  
; Sequence 9, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198.806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-198-806C-9

Query Match 100.0%; Score 22; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
||||  
Db 1 DRVY 4

## RESULT 15

US-09-352-191-9  
; Sequence 9, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue  
; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352.191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)  
US-09-352-191-9

Query Match 100.0%; Score 22; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
||||  
Db 1 DRVY 4

Search completed: July 1, 2002, 07:43:01  
Job time: 302 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:30 ; Search time 69.93 Seconds  
(without alignments)  
5.496 Million cell updates/sec

Title: US-09-723-197-10

Perfect score: 22

Sequence: 1 DRVY 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	100.0	10	2 A60624	angiotensin I - Ja
2	22	100.0	10	2 S65432	angiotensin I - ho
3	22	100.0	10	2 A90917	angiotensin precu
4	22	100.0	10	2 A90345	angiotensin precu
5	22	100.0	14	2 A01250	angiotensin precu
6	22	100.0	15	2 A60834	angiotensin I prec
7	22	100.0	43	2 S42852	meIA protein - Sal
8	22	100.0	52	2 T15646	hypothetical prote
9	22	100.0	54	2 PT0194	protein-tyrosine k
10	22	100.0	54	2 PT0189	protein-tyrosine k
11	22	100.0	74	2 H70944	hypothetical prote
12	22	100.0	84	2 A95174	hypothetical prote
13	22	100.0	84	2 B99040	hypothetical prote
14	22	100.0	88	2 E90169	hypothetical prote
15	22	100.0	92	2 T18731	hypothetical prote
16	22	100.0	99	2 C69025	conserved hypothet
17	22	100.0	101	2 G81116	hypothetical prote
18	22	100.0	113	2 PN0091	alpha-dextrin endo
19	22	100.0	113	2 A96960	hypothetical prote
20	22	100.0	115	2 A48793	glycosylation-inhi
21	22	100.0	115	2 I52370	macrophage migrati
22	22	100.0	115	2 A44499	macrophage migrati
23	22	100.0	115	2 C47274	migration inhibito
24	22	100.0	121	2 H87615	conserved hypothet
25	22	100.0	124	2 B70472	flagellar protein
26	22	100.0	124	2 E90326	hypothetical prote
27	22	100.0	126	2 S31027	gene 82 protein -
28	22	100.0	128	2 T30432	hypothetical prote
29	22	100.0	133	2 AE2202	hypothetical prote

30 22 100.0 135 2 G86695 hypothetical prote  
31 22 100.0 137 1 I40658 methylaspartate mu  
32 22 100.0 137 1 S29502 methylaspartate mu  
33 22 100.0 137 2 T41575 ubiquinol-cytochro  
34 22 100.0 139 2 E72856 Acorfi-53 protein -  
35 22 100.0 142 2 T12987 hypothetical prote  
36 22 100.0 144 2 E87693 conserved hypothet  
37 22 100.0 144 2 T22423 hypothetical prote  
38 22 100.0 146 2 T10325 hypothetical prote  
39 22 100.0 147 2 T35696 xylanase A - Strep  
40 22 100.0 157 2 G00016 FGF-receptor - com  
41 22 100.0 158 2 D90391 conserved hypothet  
42 22 100.0 159 2 F86400 hypothetical prote  
43 22 100.0 160 2 T15925 hypothetical prote  
44 22 100.0 160 2 AF2171 hypothetical prote  
45 22 100.0 161 2 AD0360 conserved hypothet

#### ALIGNMENTS

RESULT 1

A60624  
angiotensin I - Japanese quail  
C:Species: Coturnix coturnix japonica (Japanese quail)  
C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-Mar-1999  
C:Accession: A60624

R:Takei, Y.; Hasegawa, Y.

Gen. Comp. Endocrinol. 79, 12-22, 1990

A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of t

A:Reference number: A60624; MUID:90284684

A:Accession: A60624

A:Molecule type: protein

A:Residues: 1-10 <RAK>

C:Superfamily: antithrombin III

C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 100.0%; Score 22; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4

Db 1 DRVY 4

RESULT 2

S65432

angiotensin I - horn fly (fragment)

C:Species: Haematobia irritans (horn fly)

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997

C:Accession: S65432

R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen

Eur. J. Biochem. 237, 414-423, 1996

A:Title: Cloning and characterisation of angiotensin-converting enzyme from the diptre

A:Reference number: S65431; MUID:96215437

A:Accession: S65432

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <WJ>

A>Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 22; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4

Db 1 DRVY 4

RESULT 3  
A: angiotensin precursor - chicken (fragment)  
C: Species: Gallus gallus (chicken)  
C: Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C: Accession: A90917; A01250  
R: Nakayama, T.; Nakajima, T.; Sokabe, H.  
Chem. Pharm. Bull. 21, 2085-2087, 1973  
A: Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its  
A: Reference number: A90917; MUID: 74127845  
A: Accession: A90917  
A: Molecule type: protein  
A: Residues: 1-10 <NA>  
C: Keywords: blood pressure control; hormone; vasoconstrictor  
F: 1-10/Product: angiotensin I #status experimental <AN1>  
F: 1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
Db 1 DRVY 4

RESULT 4  
A: angiotensin precursor - bovine (fragment)  
C: Species: Bos primigenius taurus (cattle)  
C: Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C: Accession: A90345; A01250  
R: Elliott, D.F.; Peart, W.S.  
Biochem. J. 65, 246-254, 1957  
A: Title: The amino acid sequence in a hypertensin.  
A: Reference number: A90345  
A: Accession: A90345  
A: Molecule type: protein  
A: Residues: 1-10 <ELL>  
C: Keywords: blood pressure control; hormone; vasoconstrictor  
F: 1-10/Product: angiotensin I #status experimental <AN1>  
F: 1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
Db 1 DRVY 4

RESULT 5  
A: angiotensin precursor - horse (fragment)  
C: Species: Equus caballus (domestic horse)  
C: Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998  
C: Accession: A92775; A01250  
R: Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957  
A: Reference number: A92775  
A: Accession: A92775  
A: Molecule type: protein  
A: Residues: 1-14 <SKE>  
C: Superfamily: antithrombin III  
C: Keywords: blood pressure control; hormone; vasoconstrictor  
F: 1-10/Product: angiotensin I #status experimental <AN1>  
F: 1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 22; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
Db 1 DRVY 4

Best Local Similarity 100.0%; Pred. No. 20;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
Db 1 DRVY 4

RESULT 6  
A: angiotensin I precursor - dog (fragment)  
N: Alternate names: angiotensinogen I  
N: Contains: angiotensin I  
C: Species: Canis lupus familiaris (dog)  
C: Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1998  
C: Accession: A60834  
R: Oliver, J.A.  
Hypertension 11, 21-27, 1988  
A: Title: Purification and partial characterization of canine angiotensinogen.  
A: Reference number: A60834; MUID: 88113996  
A: Accession: A60834  
A: Molecule type: protein  
A: Residues: 1-15 <OLI>  
C: Superfamily: antithrombin III  
C: Keywords: glycoprotein; plasma  
F: 1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 22; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
Db 1 DRVY 4

RESULT 7  
S42852  
A: melA protein - Salmonella typhimurium (fragment)  
C: Species: Salmonella typhimurium  
C: Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 22-Jun-1999  
C: Accession: S42852  
R: Mizushima, K.; Awakihara, S.; Kuroda, M.; Tsuda, M.; Tsuchiya, T.  
Mol. Gen. Genet. 234, 74-80, 1992  
A: Title: Cloning and sequencing of the melB gene encoding the melibiose permease of S.  
A: Reference number: S23576; MUID: 92357019  
A: Accession: S42852  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-43 <MIZ>  
A: Cross-references: EMBL:X62101; NID:g450672; PIDN:CAA44010.1; PID:g450673  
C: Superfamily: melibiose-specific alpha-galactosidase

Query Match 100.0%; Score 22; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
Db 1 DRVY 4

RESULT 8  
T15646  
A: hypothetical protein C36F1.10 - Caenorhabditis elegans  
C: Species: Caenorhabditis elegans  
C: Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C: Accession: T15646  
R: Geisel, C.; Stellyes, L.; Bradshaw, H.  
Submitted to the EMBL Data Library, March 1996  
A: Description: The sequence of C. elegans cosmid C26F1.

A:Reference number: Z18381  
A:Accession: T15646  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-52 <GEI>  
A:Cross-references: EMBL:U53148; NID:g1255375; PID:g1255385; PIDN:AAB37072.1; GSPDB:GN00164  
A:Experimental source: strain Bristol N2; clone C26F1  
C:Genetics:  
A:Gene: CESP:C26F1.10  
A:Map position: 5  
A:Introns: 29/1

Query Match 100.0%; Score 22; DB 2; Length 52;

Best Local Similarity 100.0%; Pred. No. 78;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

||||

Db 41 DRVY 44

RESULT 9

PT0194

protein-tyrosine kinase (EC 2.7.1.112) tyro-12 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 10-Sep-1997

C:Accession: PT0194

R:Lai, C.; Lemke, G.

Neuron 6, 691-704, 1991

A:Title: An extended family of protein-tyrosine kinase genes differentially expressed in

A:Reference number: PT0183; MUID:91222560

A:Accession: PT0194

A:Molecule type: mRNA

A:Residues: 1-54 <LAI>

A:Experimental source: sciatic nerve

C:Genetics:

A:Gene: tyro-12

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F.1-54/Domain: protein kinase homology (fragment) <KIN>

Query Match 100.0%; Score 22; DB 2; Length 54;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

||||

Db 47 DRVY 50

RESULT 10

PT0189

protein-tyrosine kinase (EC 2.7.1.112) tyro-7 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 04-Feb-2000

C:Accession: PT0189

R:Lai, C.; Lemke, G.

Neuron 6, 691-704, 1991

A:Title: An extended family of protein-tyrosine kinase genes differentially expressed in

A:Reference number: PT0183; MUID:91222560

A:Accession: PT0189

A:Molecule type: mRNA

A:Residues: 1-54 <LAI>

A:Experimental source: sciatic nerve

C:Genetics:

A:Gene: tyro-7

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F.1-54/Domain: protein kinase homology (fragment) <KIN>

Query Match 100.0%; Score 22; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

||||

Db 47 DRVY 50

RESULT 11

H70944

hypothetical protein RV2049c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: H70944

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987

A:Accession: H70944

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-74 <COL>

A:Cross-references: GB:AL021899; GB:AL123456; NID:g3242282; PIDN:CAA17263.1; PID:e125

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2049c

Query Match 100.0%; Score 22; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

||||

Db 27 DRVY 30

RESULT 12

A95174

hypothetical protein SP1494 [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C:Accession: A95174

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: A95174

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-84 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK75586.1; PID:g14972984; GSPDB:GN00164; TIGR:

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1494

Query Match 100.0%; Score 22; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

||||

Db 66 DRVY 69

## RESULT 13

B99040  
hypothetical protein spr1347 [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C:Accession: B99040  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: B99040  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-84 <KUF>  
A:Cross-references: GB:AE007317; PIDN:AAL00151.1; PID:gl5458994; GSPDB:GN00174  
C:Genetics:  
A:Gene: spr1347

Query Match 100.0%; Score 22; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
DB 66 DRVY 69

## RESULT 14

B90169  
hypothetical protein SS05544 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C:Accession: E90169  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: E90169  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <KUF>  
A:Cross-references: GB:AE006641; NID:gl3813414; PIDN:AAK40612.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: SS05544

Query Match 100.0%; Score 22; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
||||  
DB 84 DRVY 87

## RESULT 15

T18731  
hypothetical protein B0391.10 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T18731  
R:Gardner, A.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19012  
A:Accession: T18731  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:09 ; Search time 34.05 Seconds  
(without alignments)  
4.549 Million cell updates/sec

Title: US-09-723-197-10  
Perfect score: 22  
Sequence: 1 DRVY 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	100.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
2	22	100.0	10	1 ANGL_BOTJA	Q10581 bothrops ja
3	22	100.0	10	1 ANGT_BOVIN	P01017 bos taurus
4	22	100.0	10	1 ANGT_CHICK	P01018 gallus gall
5	22	100.0	14	1 ANGT_HORSE	P01016 equus cabal
6	22	100.0	99	1 YB87_METH	O27255 methanobact
7	22	100.0	114	1 MIF_CHICK	O29260 gallus gall
8	22	100.0	114	1 MIF_HUMAN	P14174 homo sapien
9	22	100.0	114	1 MIF_MOUSE	P34884 mus musculu
10	22	100.0	114	1 MIF_RAT	P30904 rattus norv
11	22	100.0	126	1 VG82_BPML5	Q05298 mycobacteri
12	22	100.0	137	1 MAMA_CLOCO	P80078 clostridium
13	22	100.0	137	1 MAMA_CLOTT	Q05488 clostridium
14	22	100.0	137	1 UCR7_SCHPO	O74533 schizosacch
15	22	100.0	139	1 Y053_NPVAC	P41457 autographa
16	22	100.0	146	1 Y053_NPVOP	Q10310 orgyia pseu
17	22	100.0	161	1 RNPA_HELPJ	Q22jho helicobacte
18	22	100.0	161	1 RNPA_HELPY	P35997 helicobacte
19	22	100.0	162	1 MCRW_METH	Q05485 methanobact
20	22	100.0	174	1 YA68_METH	O27140 methanobact
21	22	100.0	177	1 Y552_TREPA	O83563 treponema p
22	22	100.0	178	1 NADM_METH	Q06253 methanobact
23	22	100.0	181	1 NIP7_YEAST	O08962 saccharomyc
24	22	100.0	183	1 SOMA_PRIGL	P34006 prionace gl
25	22	100.0	190	1 SOMA_BALBO	P33092 balaenopter
26	22	100.0	190	1 SOMA_LAMPA	P37885 lama guanac
27	22	100.0	190	1 SOMA_LOXAF	P20392 loxodonta a
28	22	100.0	190	1 SOMA_VULVU	P10766 vulpes vulp
29	22	100.0	191	1 SOMA_CHEMY	P34005 chelonias my
30	22	100.0	201	1 ARA5_ARAHY	P04149 arachis hyp
31	22	100.0	215	1 SOMA_MONDO	Q9g160 monodelphis
32	22	100.0	215	1 SOMA_RANCA	P10813 rana catesb
33	22	100.0	215	1 SOMA_TRIVU	O62754 trichosurus

34	22	100.0	216	1 SOMA_CANFA	P33711 canis famil
35	22	100.0	216	1 SOMA_FELCA	P46404 felis silve
36	22	100.0	216	1 SOMA_HORSE	P01245 equus cabal
37	22	100.0	216	1 SOMA_MESAU	P37886 mesocricetu
38	22	100.0	216	1 SOMA_MOUSE	P06880 mus musculu
39	22	100.0	216	1 SOMA_MUSVI	P19795 mustela vis
40	22	100.0	216	1 SOMA_PIG	P01248 sus scrofa
41	22	100.0	216	1 SOMA_RABIT	P46407 oryctolagus
42	22	100.0	216	1 SOMA_RAT	P01244 rattus norv
43	22	100.0	217	1 SOMA_BOVIN	P01246 bos taurus
44	22	100.0	217	1 SOMA_BUBBU	O18938 bubalus bub
45	22	100.0	217	1 SOMA_CEREL	P56437 cervus elap

ALIGNMENTS

RESULT 1  
ANG2\_BOTJA  
ID ANG2\_BOTJA STANDARD; PRT; 8 AA.  
AC Q10582;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide II (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
RT "Isolation and identification of angiotensin-like peptides from the  
plasma of the snake Bothrops jararaca".  
RL Comp. Biochem. Physiol. 113B:467-473(1996).  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
DR Vasoconstrictor; Plasma; Serpin.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 22; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
Db 1 DRVY 4

RESULT 2  
ANGL\_BOTJA  
ID ANGL\_BOTJA STANDARD; PRT; 10 AA.  
AC Q10581;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide I (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca.";  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
 ||||  
 Db 1 DRVY 4

RESULT 3  
 ANGT\_BOVIN STANDARD; PRT; 10 AA.  
 ID ANGT\_BOVIN  
 AC P01017;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN8 OR AGT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RA Elliott D.F., Peart W.S.;  
 RT "The amino acid sequence in a hypertensin.";  
 RL Biochem. J. 65:246-254(1957).  
 CC -I- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -I- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR; A01250; A01250.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1282 MW; CEEFDD761F2DB42 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
 ||||  
 Db 1 DRVY 4

RESULT 4  
 ANGT\_CHICK STANDARD; PRT; 10 AA.  
 ID ANGT\_CHICK  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN8 OR AGT.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 93934;  
 RN [1]  
 RP SEQUENCE.

RC SPECIES=C.G.japonica;  
 RX MEDLINE=90284684; PubMed=2191893;  
 RA Takei Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and  
 RT inhibition of these effects in the Japanese quail.";  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -I- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -I- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR; A01250; A01250.  
 DR PIR; A90917; A90917.  
 DR PIR; A60624; A60624.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; CEFBDD761F2DB42 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
 ||||  
 Db 1 DRVY 4

RESULT 5  
 ANGT\_HORSE STANDARD; PRT; 14 AA.  
 ID ANGT\_HORSE  
 AC P01016;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN8 OR AGT.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE.

RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;  
 RT "The preparation, purification, and amino acid sequence of a  
 RT polypeptide renin substrate";  
 RL J. Exp. Med. 106:439-453(1957).

CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR: A01250; A01250.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBDD7 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
DB 1 DRVY 4

RESULT 6  
YB87\_MEETH STANDARD; PRT; 99 AA.  
AC 027255;

DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein MTH1187.

GN Methanobacterium thermoautotrophicum.  
OS Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;  
OC Methanothermobacter.  
OX NCBI\_TaxID=145262;

RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=DELTA H;  
RX MEDLINE=98037514; PubMed=9371463;  
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RA "Complete genome sequence of Methanobacterium thermoautotrophicum  
RT delah: functional analysis and comparative genomics."  
RL J. Bacteriol. 179:7135-7155(1997).  
CC -!- SIMILARITY: BELONGS TO THE UPF0045 FAMILY.

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DR EMBL; A000887; AAB85676.1; -  
DR InterPro: IPR002767; DUF77.  
DR Pfam; PF01910; DUF77; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 99 AA; 10798 MW; 32D48B66A74C7430 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 54;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVY 4  
DB 70 DRVY 73

RESULT 7

MIF\_CHICK STANDARD; PRT; 114 AA.  
AC Q02960;

DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate  
DE tautomerase).  
GN MIF.

OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;

RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Lens;  
RX MEDLINE=93165679; PubMed=7679497;  
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;

RA "A macrophage migration inhibitory factor is expressed in the  
RT differentiating cells of the eye lens."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).

CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A  
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN  
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.

CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M95776; AAA48939.1; -  
DR PIR; C47274; C47274.

DR HSP; P34884; IMFI.

DR InterPro: IPR001398; MIF.

DR Pfam; PF01187; MIF; 1.

DR PROSITE: PS01158; MIF; 1.

DR Isomerase; Macrophage; Inflammatory response; Cytokine.

FT ACI\_SITE 1 1 CATALYTIC BASE (BY SIMILARITY).

FT INT\_MET 0 0 BY SIMILARITY.

SQ SEQUENCE 114 AA; 12353 MW; A5522D00E6D05CF CRC64;

Query Match 100.0%; Score 22; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
DB 92 DRVY 95

RESULT 8

MIF\_HUMAN STANDARD; PRT; 114 AA.  
AC P14174;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate

DE tautomerase) (Glycosylation-inhibiting factor) (GIF).  
GN MIF OR MMIF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=90017510; PubMed=2552447;  
RA Weiser W.Y., Temple P.A., Witek-Giannotti J.S., Remold H.G.,  
RA Clark S.C., David J.R.;  
RA "Molecular cloning of a cDNA encoding a human macrophage migration  
RT inhibitory factor.";  
RT Proc. Natl. Acad. Sci. U.S.A. 86:7522-7526(1989).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=94245178; PubMed=8188240;  
RA Paralikar V., Wistow G.J.;  
RA "Cloning the human gene for macrophage migration inhibitory factor  
RT (MIF).";  
RT Genomics 19:48-51(1994).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=94052102; PubMed=8234256;  
RA Miyayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C.,  
RA Iwamatsu A., Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;  
RA "Molecular cloning and functional expression of a cDNA encoding  
RT glycosylation-inhibiting factor.";  
RT Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).  
RN [4]  
RN SEQUENCE OF 9-114 FROM N.A.  
RC TISSUE=Lens;  
RX MEDLINE=93165679; PubMed=7679497;  
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;  
RA "A macrophage migration inhibitory factor is expressed in the  
RT differentiating cells of the eye lens.";  
RT Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).  
RN [5]  
RN SEQUENCE OF 1-10.  
RC TISSUE=Liver;  
RX MEDLINE=93162045; PubMed=1286669;  
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
RA Appel R.D., Hughes G.J.;  
RA "Human liver protein map: a reference database established by  
RT microsequencing and gel comparison.";  
RL Electrophoresis 13:992-1001(1992).  
RN [6]  
RN SEQUENCE OF 2-23.  
RX MEDLINE=93256574; PubMed=7683862;  
RA Zeng F.Y., Weiser W.Y., Kratzin H., Stahl B., Karas M., Gabius H.J.;  
RA "The major binding protein of the interferon antagonist sarcolectin  
RT in human placenta is a macrophage migration inhibitory factor.";  
RL Arch. Biochem. Biophys. 303:74-80(1993).  
RN [7]  
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RP MEDLINE=96338096; PubMed=8766818;  
RA Sugimoto H., Suzuki M., Nakagawa A., Tanaka I., Nishihira J.;  
RA "Crystal structure of macrophage migration inhibitory factor from  
RT human lymphocyte at 2.1-A resolution.";  
RL FEBS Lett. 389:145-148(1996).  
RN [8]  
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RP MEDLINE=96181524; PubMed=8610159;  
RA Kato Y., Muto T., Tomura T., Tsumura H., Watarai H., Miyayama T.,  
RA Ishizaka K., Kuroki R.;  
RA "The crystal structure of human glycosylation-inhibiting factor is a  
RT trimeric barrel with three 6-stranded beta-sheets.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:3007-3010(1996).  
RN [9]  
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RP MEDLINE=96224258; PubMed=8643551;  
RA Sun H.W., Bernhagen J., Bucala R., Lolis E.;  
RA "Crystal structure at 2.6-A resolution of human macrophage migration  
RT inhibitory factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:5191-5196(1996).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RP MEDLINE=99282199; PubMed=10353846;  
RA Lubetsky J.B., Swope M., Dealwis C., Blake P., Lolis E.;  
RA "Pro-1 of macrophage migration inhibitory factor functions as a  
RT catalytic base in the phenylpyruvate tautomerase activity.";  
RT Biochemistry 38:7346-7354(1999).  
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A  
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN  
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.  
CC -!- SUBUNIT: HOMOTRIMER.  
CC -!- DISEASE: MIF ACTIVITY HAS BEEN DETECTED IN LEUKOCYTE CULTURE  
CC SUPERNATANTS OF MICE DURING ALLOGRAFT REJECTION, IN THE SYNOVIA  
CC OF PATIENTS WITH RHEUMATOID POLYARTHRITIS, AND IN A VARIETY OF  
CC CHRONIC INFLAMMATORY LOCI.  
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.  
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CC -----  
DR EMBL; Z23063; CAA80598.1; -;  
DR EMBL; Z25639; AAA36315.1; -;  
DR EMBL; M95775; AAA36179.1; -;  
DR EMBL; L10612; AAA35892.1; -;  
DR EMBL; L19686; AAA21814.1; -;  
DR PIR; A33838; A33838.  
DR PIR; S33277; S33277.  
DR PDB; 1GIF; 12-MAR-96.  
DR PDB; 1MIF; 07-DEC-96.  
DR PDB; 1PIG; 07-JUN-99.  
DR PDB; 1CGQ; 07-JUN-99.  
DR PDB; 1CA7; 30-JUN-99.  
DR SWISS-2DPAGE; P14174; HUMAN.  
DR Slen-2DPAGE; P14174; -;  
DR MIM; 153620; -;  
DR InterPro; IPR001398; MIF.  
DR Pfam; PF01187; MIF; 1.  
DR PROSITE; PS01158; MIF; 1.  
KW Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.  
FT INIT\_MET 0  
FT ACT\_SITE 1 1 CATALYTIC BASE.  
FT CONFLICT 105 105 N -> S (IN REF. 1).  
SQ SEQUENCE 114 AA; 12345 MW; 4BD52532B3F3069 CRC64;  
Query Match 100.0%; Score 22; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVY 4  
DB 92 DRVY 95  
RESULT 9  
MIF\_MOUSE  
ID MIF\_MOUSE STANDARD; PRT; 114 AA.  
AC P34884;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate  
DE tautomerase) (Delayed early response protein 6) (DER6) (Glycosylation-  
DE inhibiting factor).  
GN MIF.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.  
 RC TISSUE=Pituitary;  
 RX MEDLINE=94019845; PubMed=8413654;  
 RA Bernhagen J., Calandra T., Mitchell R.A., Martin S.B.,  
 RA Tracey K.J., Voelter W., Manogue K.R., Cerami A., Bucala R.;  
 RT "MIF is a pituitary-derived cytokine that potentiates lethal  
 RT endotoxaemia.";  
 RL Nature 365:756-759(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=92375060; PubMed=1508193;  
 RA Lanahan A., Williams J.B., Sanders L.K., Nathans D.;  
 RA "Growth factor-induced delayed early response genes";  
 RT Mol. Cell. Biol. 12:3919-3929(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94052102; PubMed=8234256;  
 RA Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C., Iwamatsu A.,  
 RA Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;  
 RT "Molecular cloning and functional expression of a cDNA encoding  
 RT glycosylation-inhibiting factor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=95221891; PubMed=7706726;  
 RA Mitchell R., Bacher M., Bernhagen J., Pushkarskaya T., Seldin M.F.,  
 RA Bucala R.;  
 RT "Cloning and characterization of the gene for mouse macrophage  
 RT migration inhibitory factor (MIF)";  
 RL J. Immunol. 154:3863-3870(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=96047325; PubMed=7558021;  
 RA Bozza M., Kolakowski L.F. Jr., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., David J.R., Gerard C.;  
 RT "Structural characterization and chromosomal location of the mouse  
 RT macrophage migration inhibitory factor gene and pseudogenes";  
 RL Genomics 27:412-419(1995).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=96047324; PubMed=7558020;  
 RA Kozak C.A., Adamson M.C., Buckler C.E., Segovia L., Paralkar V.,  
 RA Wistow G.;  
 RT "Genomic cloning of mouse MIF (macrophage inhibitory factor) and  
 RT genetic mapping of the human and mouse expressed gene and nine mouse  
 RT pseudogenes";  
 RL Genomics 27:405-411(1995).  
 RN [7]  
 RP SEQUENCE OF 5-114 FROM N.A.  
 RC TISSUE=Lens;  
 RX MEDLINE=93165679; PubMed=7679497;  
 RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;  
 RT "A macrophage migration inhibitory factor is expressed in the  
 RT differentiating cells of the eye lens";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RX MEDLINE=99303983; PubMed=10360941;  
 RA Taylor A.B., Johnson W.H. Jr., Czerwinski R.M., Li H.S., Hackert M.L.,  
 RA Whitman C.P.;  
 RT "Crystal structure of macrophage migration inhibitory factor  
 RT complexed with (E)-2-fluoro-p-hydroxycinnamate at 1.8 A resolution:  
 RT implications for enzymatic catalysis and inhibition";  
 RL Biochemistry 38:7444-7452(1999).

RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS).  
 RX MEDLINE=20393856; PubMed=10933783;  
 RA Stamps S.L., Taylor A.B., Wang S.C., Hackert M.L., Whitman C.P.;  
 RT "Mechanism of the phenylpyruvate tautomerase activity of macrophage  
 RT migration inhibitory factor: properties of the PLG, P1A, Y95F, and  
 RT N97A mutants";  
 RL Biochemistry 39:9671-9678(2000).  
 CC [1]- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A  
 CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN  
 CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.  
 CC [2]- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
 CC [3]- SIMILARITY: BELONGS TO THE MIF FAMILY.  
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 CC  
 CC EMBL; Z23048; CAA80583.1; -  
 CC EMBL; U19825; AAA91637.1; -  
 CC EMBL; L10613; AAA37693.1; -  
 CC EMBL; U20156; AAA91638.1; -  
 CC EMBL; L39357; AAA74321.1; -  
 CC EMBL; L07607; AAA37111.1; -  
 CC PIR; S34299; S34299.  
 CC PIR; A44499; A44499.  
 CC PDB; 1MFF; 11-AUG-00.  
 CC PDB; 1MFI; 22-JUN-99.  
 CC MGD; MGI:96982; Mif.  
 CC InterPro; IPR001398; MIF.  
 CC Pfam; PF01187; MIF; 1.  
 CC PROSITE; PS01158; MIF; 1.  
 CC Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.  
 KW INIT\_MET 0  
 FT ACT\_SITE 1 1 CATALYTIC BASE.  
 SQ SEQUENCE 114 AA; 12373 MW; 8FD2339CF0792F9E CRC64;  
  
 Query Match 100.0%; Score 22; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 DRVY 4  
 Db 92 DRVY 95  
 ||||  
  
 RESULT 10  
 MIF\_RAT  
 ID MIF\_RAT STANDARD; PRT: 114 AA.  
 AC P30904;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate  
 DE tautomerase) (Glutathione-binding 13 kDa protein).  
 GN MIF.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=95038523; PubMed=7951062;  
 RT "Glutathione binding rat liver 13k protein is the homologue of the  
 RT macrophage migration inhibitory factor";  
 RL Biochem. Mol. Biol. Int. 33:439-446(1994).

GN 82. Gene 82 protein (GP82).  
OS Mycobacteriophage L5.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=31757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93211282; PubMed=8459766;  
RA Hatfull G.F., Sarkis G.J.;  
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
a phage system for mycobacterial genetics.";  
RL Mol. Microbiol. 7:395-405(1993).  
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CC -----  
DR EMBL; Z18946; CAA79458.1; -  
DR PIR; S31027; S31027.  
SQ SEQUENCE 126 AA; 14167 MW; 7D1188C3B2CAC8C6 CRC64;  
  
Query Match 100.0%; Score 22; DB 1; Length 126;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVY 4  
DB 114 DRVY 117  
  
RESULT 12  
MAMA\_CLOCO  
ID MAMA\_CLOCO STANDARD; PRT; 137 AA.  
AC P80078; Q60144;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Methylaspartate mutase S chain (EC 5.4.99.1) (Glutamate mutase sigma  
DE subunit).  
GN MAMA OR GLMS.  
OS Clostridium cochlearium.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1494;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 1285 / ATCC 17787;  
RX MEDLINE=95094816; PubMed=7880251;  
RA Zelder O., Beatrix B., Leutbecher U., Buckel W.;  
RT "Characterization of the coenzyme-B12-dependent glutamate mutase from  
RT Clostridium cochlearium produced in Escherichia coli.";  
RL Eur. J. Biochem. 226:577-585(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 1285 / ATCC 17787;  
RX MEDLINE=94283856; PubMed=8013871;  
RA Zelder O., Beatrix B., Buckel W.;  
RT "Cloning, sequencing and expression in Escherichia coli of the gene  
RT encoding component S of the coenzyme B12-dependent glutamate mutase  
RT from Clostridium cochlearium.";  
RL FEMS Microbiol. Lett. 118:15-21(1994).  
RN [3]  
RP SEQUENCE OF 1-23.  
RC STRAIN=DSM 1285 / ATCC 17787;  
RX MEDLINE=92241315; PubMed=1315276;  
RA Leutbecher U., Boeher R., Linder D., Buckel W.;  
RT "Glutamate mutase from Clostridium cochlearium. Purification,  
RT cobamide content and stereospecific inhibitors.";

DE SEQUENCE FROM N.A.  
GN TISSUE=Lens;  
RA Wen Y., Li G., Bekhor I.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=PVG/C;  
RA Sleeman M.A., Huckle J.W., Robinson M., Jahoda C.A.B.,  
RA Reynolds A.J., Whitehouse C.J.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-25.  
RX MEDLINE=93063370; PubMed=1436109;  
RA Blocki F.A., Schlievert P.M., Wackett L.P.;  
RT "Rat liver protein linking chemical and immunological detoxification  
RT systems.";  
RL Nature 360:269-270(1992).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RC TISSUE=Liver;  
RX MEDLINE=96186248; PubMed=8605628;  
RA Suzuki M., Sugimoto H., Nakagawa A., Tanaka I., Nishihira J.,  
RA Sakai M.;  
RT "Crystal structure of the macrophage migration inhibitory factor from  
RT rat liver.";  
RL Nat. Struct. Biol. 3:259-266(1996).  
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A  
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN  
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.  
CC -!- SUBUNIT: HOMOTRIMER.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF ORGANS  
CC INCLUDING BRAIN, SPLEEN, LIVER, MUSCLE AND KIDNEY.  
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.  
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CC -----  
DR EMBL; S73424; AAB32392.1; -  
DR EMBL; U20999; AAG2644.1; -  
DR EMBL; U62326; AAB04024.1; -  
DR PDB; 1FIM; 11-JUL-96.  
DR InterPro; IPR001398; MIF.  
DR Pfam; PF01187; MIF; 1.  
DR PROSITE; PS01158; MIF; 1.  
KW Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.  
FT INIT\_MET 0 0  
FT ACT\_SITE 1 1 CATALYTIC BASE (BY SIMILARITY).  
FT CONFLICT 50 50 S -> R (IN REF. 2).  
SQ SEQUENCE 114 AA; 12346 MW; 9E33C39CF064329E CRC64;  
  
Query Match 100.0%; Score 22; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRVY 4  
DB 92 DRVY 95  
  
RESULT 11  
VG82\_BPML5  
ID VG82\_BPML5 STANDARD; PRT; 126 AA.  
AC Q05298;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)



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RL Eur. J. Biochem. 205:759-765(1992).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RC STRAIN=DSM 1285 / ATCC 17787;
RX MEDLINE=99404935; PubMed=10467146;
RA Reitzer R., Gruber K., Jogi G., Wagner U.G., Bothe H., Buckel W.,
RT Kratky C.;
RA "Glutamate mutase from Clostridium cochlearium: the structure of a
RT coenzyme B12-dependent enzyme provides new mechanistic insights.";
RL Structure 7:891-902(1999).
CC -i- CATALYTIC ACTIVITY: L-threo-3-methylaspartate = L-glutamate.
CC -i- COFACTOR: 5'-deoxy-5'-adenosyl-adeninylcobamide (pseudo-coenzyme
CC B12).
CC -i- PATHWAY: Fermentation of glutamate; first step.
CC -i- SUBUNIT: Heterotetramer of 2 E subunits and 2 S subunits.
CC -i- SIMILARITY: CONTAINS 1 B12-BINDING DOMAIN.
CC -----
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CC -----
DR EMBL; X80997; CAA56921.1; -.
DR EMBL; X75890; CAA53484.1; -.
DR PIR; S21249; S21249.
DR PDB; 1CB7; 28-FEB-00.
DR PDB; 1CCW; 01-MAR-00.
DR InterPro; IPR003312; B12-binding.
DR Pfam; PF02310; B12-binding; 1.
DR Isomerase; Cobalt; Vitamin B12; 3D-structure.
DR METAL 16 CORALT.
FT SEQUENCE 137 AA; 14812 MW; D9C5BF8DE5D1E878 CRC64;
SQ

Query Match 100.0%; Score 22; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4
DB 114 DRVY 117

RESULT 13
MAMA_CLOTT
ID MAMA_CLOTT STANDARD; PRT; 137 AA.
AC Q05488;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Methylaspartate mutase S chain (EC 5.4.99.1) (Glutamate mutase sigma
DE subunit).
DE MAMA OR MUTS.
GN Clostridium tetanomorphum.
OS Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1553;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-33.
RC STRAIN=NCIMB 11547;
RX MEDLINE=93011908; PubMed=1397267;
RA Marsh E.N.G., Holloway D.E.;
RT "Cloning and sequencing of glutamate mutase component S from
RT Clostridium tetanomorphum. Homologies with other cobalamin-dependent
RT enzymes.";
RL FEBS Lett. 310:167-170(1992).
RN [2]
RP SEQUENCE OF 1-24.
RC STRAIN=H1 / DSM 528;
RX MEDLINE=93202282; PubMed=8454064;
```

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RA Brecht M., Kellermann J., Plueckthun A.;
RT "Cloning and sequencing of glutamate mutase component E from
RT Clostridium tetanomorphum.";
RL FEBS Lett. 319:84-89(1993).
RN [3]
RP STRUCTURE BY NMR.
RC STRAIN=ATCC 15920;
RX MEDLINE=98416697; PubMed=9739092;
RA Tollinger M., Konrat R., Hilbert B.H., Marsh E.N.G., Kraeutler B.;
RT "How a protein prepares for B12 binding: structure and dynamics of
RT the B12-binding subunit of glutamate mutase from Clostridium
RT tetanomorphum.";
RL Structure 6:1021-1033(1998).
CC -i- CATALYTIC ACTIVITY: L-threo-3-methylaspartate = L-glutamate.
CC -i- COFACTOR: 5'-deoxy-5'-adenosyl-adeninylcobamide (pseudo-coenzyme
CC B12).
CC -i- PATHWAY: Fermentation of glutamate; first step.
CC -i- SUBUNIT: Heterotetramer of 2 E subunits and 2 S subunits. E exists
CC as a homodimer and S as a monomer.
CC -i- SIMILARITY: CONTAINS 1 B12-BINDING DOMAIN.
CC -----
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CC -----
DR EMBL; X70499; CAA49908.1; -.
DR EMBL; X68570; CAA48567.1; -.
DR PIR; S29502; S29502.
DR PDB; 1BE1; 26-AUG-98.
DR InterPro; IPR003312; B12-binding.
DR Pfam; PF02310; B12-binding; 1.
DR Isomerase; Cobalt; Vitamin B12; 3D-structure.
KW SEQUENCE 137 AA; 14748 MW; E71FE55BA8CE3DB3 CRC64;
SQ

Query Match 100.0%; Score 22; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4
DB 114 DRVY 117

RESULT 14
UCR7_SCHPO
ID UCR7_SCHPO STANDARD; PRT; 137 AA.
AC 074533;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ubiquinol-cytochrome C reductase complex 14 kDa protein
DE (EC 1.10.2.2) (Complex III subunit VII).
GN SPCC737.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Murphy L., Harris D., Lynne M.H., Rajandream M.A., Barrell B.G.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -i- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C
CC REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH
CC IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN. THIS COMPONENT
CC IS INVOLVED IN REDOX-LINKED PROTON PUMPING (BY SIMILARITY).
CC -i- CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
```

CC ferrocytochrome c.  
CC -!- SUBUNIT: FUNGI BC1 COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY  
CC SUBUNITS, 2 CORE PROTEINS AND 5 LOW-MOLECULAR WEIGHT PROTEINS (BY  
CC SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (Potential).  
CC -!- SIMILARITY: BELONGS TO THE UQCRB/UQR7 FAMILY.  
CC -----  
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CC -----  
CC EMBL; AL031546; CAA20859.1; -;  
CC InterPro; IPR003197; UCR\_14kD.  
CC Pfam; PF02271; UCR\_14kD; 1.  
CC Mitochondrion; Inner membrane; Electron transport; Respiratory chain;  
KW Oxidoreductase.  
SQ SEQUENCE 137 AA; 16030 MW; 36CEFF418C9E02994 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 137;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
DB 65 DRVY 68  
||||

RESULT 15  
Y053\_NPVAC STANDARD; PRT; 139 AA.  
AC P41457;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Hypothetical 17.0 kDa protein in LEF8-FP intergenic region.  
OS Autographa californica nuclear polyhedrosis virus (ACMNPV).  
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
OC Nucleopolyhedrovirus.  
OX NCBI\_TaxID=46015;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C6;  
RX MEDLINE=94303173; PubMed=8030224;  
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;  
RT "The complete DNA sequence of Autographa californica nuclear  
RT polyhedrosis virus."  
RL Virology 202:586-605(1994).  
CC -!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.  
CC -----  
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CC -----  
CC EMBL; L22858; AAA66683.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 139 AA; 16995 MW; C03632331F01EA3A CRC64;

Query Match 100.0%; Score 22; DB 1; Length 139;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
DB 65 DRVY 68  
||||

DB 109 DRVY 112

Search completed: July 1, 2002, 07:47:10  
Job time: 476 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:14 ; Search time 122.73 Seconds  
(without alignments)  
5.638 Million cell updates/sec

Title: US-09-723-197-10  
Perfect score: 22  
Sequence: 1 DRVY 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	100.0	10	13 Q9PS07	Q9ps07 alligator m
2	22	100.0	14	5 Q10757	Q10757 theromyzon
3	22	100.0	52	5 Q18234	Q18234 caenorhabdi
4	22	100.0	53	12 Q86959	Q86959 human papil
5	22	100.0	54	4 Q9UD27	Q9ud27 homo sapien
6	22	100.0	55	5 Q9TX23	Q9tx23 hirudo medi
7	22	100.0	56	13 Q91995	Q91995 xenopus lae
8	22	100.0	57	13 Q08556	Q08556 phasianidae
9	22	100.0	57	13 Q08555	Q08555 phasianidae
10	22	100.0	61	10 Q9LJ70	Q9lj70 arabidopsis
11	22	100.0	64	4 Q9NPE3	Q9npe3 homo sapien
12	22	100.0	64	5 Q9V5P6	Q9v5p6 drosophila
13	22	100.0	64	11 Q9CQS2	Q9cqs2 mus musculu
14	22	100.0	66	5 Q76159	Q76159 dugesia jap
15	22	100.0	67	13 Q90957	Q90957 gallus gall
16	22	100.0	68	13 Q9YI21	Q9yi21 gallus gall

17	22	100.0	72	2 Q9R540	Q9r540 clostridium
18	22	100.0	74	16 O53491	O53491 mycobacteri
19	22	100.0	78	11 O55059	O55059 rattus norv
20	22	100.0	82	12 Q31LD0	Q31ld0 white spot
21	22	100.0	84	16 Q97PU8	Q97pu8 streptococc
22	22	100.0	87	8 Q9G9H0	Q9g9h0 eretmoceru
23	22	100.0	88	10 Q93YK7	Q93yk7 brassica na
24	22	100.0	88	17 Q980L8	Q980l8 sulfolobus
25	22	100.0	89	10 Q94H51	Q94h51 oryza sativ
26	22	100.0	91	10 Q9FIY3	Q9fiy3 arabidopsis
27	22	100.0	91	17 Q975V9	Q975v9 sulfolobus
28	22	100.0	92	5 O62015	O62015 caenorhabdi
29	22	100.0	95	5 Q9NM38	Q9nm38 leishmania
30	22	100.0	99	15 Q907E4	Q907e4 human immun
31	22	100.0	101	16 Q9JS54	Q9js54 neisseria m
32	22	100.0	104	15 Q99CQ9	Q99cq9 human immun
33	22	100.0	104	15 Q99CN4	Q99cn4 human immun
34	22	100.0	107	15 Q97063	Q97063 chimpanzee
35	22	100.0	109	4 Q9H500	Q9h500 homo sapien
36	22	100.0	110	6 Q9N265	Q9n265 bos taurus
37	22	100.0	113	16 Q97LR6	Q97lr6 clostridium
38	22	100.0	115	12 Q91I61	Q91i61 regina rana
39	22	100.0	119	2 Q9L5D3	Q9l5d3 comamonas t
40	22	100.0	120	6 Q97SG0	Q9tsg0 ovis aries
41	22	100.0	120	16 Q98EF4	Q98ef4 rhizobium l
42	22	100.0	121	11 Q9CVB5	Q9cvb5 mus musculu
43	22	100.0	121	16 Q9A481	Q9a481 caulobacter
44	22	100.0	122	2 Q46219	Q46219 clostridium
45	22	100.0	124	16 O67806	O67806 aquifex aeo

#### ALIGNMENTS

RESULT 1

ID Q9PS07 PRELIMINARY; PRT; 10 AA.  
AC Q9PS07;  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)  
DE ANGIOTENSIN I, ANG I.  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93307610; PubMed=8319878;  
RA Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,  
RA Stephens G.A., Sakakibara S.;  
RT "New angiotensin I isolated from a reptile, Alligator  
mississippiensis.";  
RL Gen. Comp. Endocrinol. 90:214-219(1993).  
SQ SEQUENCE 10 AA; 1216 MW; CEE38DD761F2DB42 CRC64;

Query Match 100.0%; Score 22; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4

DB 1 DRVY 4

RESULT 2

ID Q10757 PRELIMINARY; PRT; 14 AA.  
AC Q10757;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)

DE ANGIOTENSINOGEN (FRAGMENT).  
OS Theromyzon tessulatum (Leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
OX NCBI\_TaxID=13286;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95365039; PubMed=7637887;  
RA Laurent V., Bulet P., Salzet M.A.;  
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like  
RT molecule with forms of vertebrate angiotensinogens: a hormonal system  
RT conserved in the course of evolution."  
RL Neurosci. Lett. 190:173-178(1995).  
RN [2]  
RP SEQUENCE OF 1-10.  
RC TISSUE=BRAIN;  
RX MEDLINE=96201949; PubMed=8612806;  
RA Laurent V., Salzet M.;  
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon  
RT tessulatum."  
RL FEBS Lett. 384:123-127(1996).  
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.  
KW Glycoprotein; Serpin.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEFBD7 CRC64;  
  
Query Match 100.0%; Score 22; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 40; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;  
Qy 1 DRVY 4  
Db 1 DRVY 4  
  
RESULT 3  
Q18234 PRELIMINARY; PRT; 52 AA.  
ID Q18234;  
AC Q18234;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE C26F1.10 PROTEIN.  
GN C26F1.10.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peleoderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Smauldson N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans".  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Geisel C., Stellies L., Bradshaw H.;  
RT "The sequence of C. elegans cosmid C26F1."  
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]

RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Waterston R.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U53148; AAB37072.1; -. 5D5D734A309F1F2 CRC64;  
SQ SEQUENCE 52 AA; 5932 MW; 5D5D734A309F1F2 CRC64;  
  
Query Match 100.0%; Score 22; DB 5; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DRVY 4  
Db 41 DRVY 44  
  
RESULT 4  
Q86959 PRELIMINARY; PRT; 53 AA.  
ID Q86959;  
AC Q86959;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE E1 (E1) (FRAGMENT).  
GN E1.  
OS Human papillomavirus type 2.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=35256;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L1;  
RX MEDLINE=96037380; PubMed=7473271;  
RA Padayachee A., Sanders C.M., Maitland N.J.;  
RT "A polymerase chain reaction (PCR) investigation of oral verrucae  
RT which contain HPV types 2 and 57 by in situ hybridization."  
RL J. Oral Pathol. Med. 24:329-334(1995).  
DR EMBL; S80058; AAB35445.2; -.  
FT NON\_TER 1 1  
FT NON\_TER 53 53  
SQ SEQUENCE 53 AA; 5628 MW; 8F6CCF2A510C209E CRC64;  
  
Query Match 100.0%; Score 22; DB 12; Length 53;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DRVY 4  
Db 40 DRVY 43  
  
RESULT 5  
Q9UD27 PRELIMINARY; PRT; 54 AA.  
ID Q9UD27;  
AC Q9UD27;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE AXL RECEPTOR TYROSINE KINASE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95204052; PubMed=7896447;  
RA Craven R.J., Xu L.H., Weiner T.M., Fridell Y.W., Dent G.A.,  
RA Srivastava S., Varnum B., Liu E.T., Cance W.G.;  
RT "Receptor tyrosine kinases expressed in metastatic colon cancer."  
RL Int. J. Cancer 60:791-797(1995).  
DR InterPro; IPR000719; Euk\_pkinase.

DR Pfam: PF00069; pkinase; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 SQ SEQUENCE 54 AA; 6164 MW; FE3D169C1CD954C1 CRC64;

Query Match 100.0%; Score 22; DB 4; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
 Db 47 DRVY 50

RESULT 6  
 Q9TX23 PRELIMINARY; PRT; 55 AA.  
 AC Q9TX23;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE LPTK53-PDGF RECEPTOR TYROSINE KINASE HOMOLOG.  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95330783; PubMed=7606763;  
 RA Nitabach M.N., Macagno E.R.;  
 RT "Cell- and tissue-specific expression of putative protein kinase mRNAs  
 in the embryonic leech, Hirudo medicinalis.";  
 RL Cell Tissue Res. 280:479-489(1995).  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 SQ SEQUENCE 55 AA; 6369 MW; AFED1C7D06C5785B CRC64;

Query Match 100.0%; Score 22; DB 5; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
 Db 48 DRVY 51

RESULT 7  
 Q91995 PRELIMINARY; PRT; 56 AA.  
 AC Q91995;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PROTEIN-TYROSINE KINASE (G62) (FRAGMENT).  
 GN G62 OR E7.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=83355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EMBRYO;  
 RX MEDLINE=95383727; PubMed=7655077;  
 RA Brandli A.W., Kirschner M.W.;  
 RT "Molecular cloning of tyrosine kinases in the early Xenopus embryo:  
 identification of Eck-related genes expressed in cranial neural crest  
 cells of the second (hyoid) arch.";  
 RL Dev. Dyn. 203:119-140(1995).

DR EMBL: U11730; AAA91293.1; -.  
 DR EMBL: U11720; AAA91283.1; -.  
 DR HSP: P11362; lFGK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase; Tyrosine-protein kinase.  
 FT NON\_TER 1  
 FT NON\_TER 56  
 FT NON\_TER 56  
 SQ SEQUENCE 56 AA; 6408 MW; BD31D90C5791B45F CRC64;

Query Match 100.0%; Score 22; DB 13; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
 Db 49 DRVY 52

RESULT 8  
 Q08556 PRELIMINARY; PRT; 57 AA.  
 AC Q08556;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE QUAIL DNA FOR FIBROBLAST GROWTH FACTOR RECEPTOR (CLONE H7)  
 DE (FRAGMENT).  
 OS Phasianidae.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes.  
 OX NCBI\_TaxID=9005;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93096482; PubMed=1281306;  
 RA Marcelle C., Eichmann A.;  
 RT "Molecular cloning of a family of protein kinase genes expressed in  
 the avian embryo.";  
 RL Oncogene 7:2479-2487(1992).  
 DR EMBL: X69693; CAA49363.1; -.  
 DR HSP: P11362; lFGK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Receptor; Transferase.  
 FT NON\_TER 1  
 FT NON\_TER 57  
 FT NON\_TER 57  
 SQ SEQUENCE 57 AA; 6523 MW; 8DAA6A71E3F1B45E CRC64;

Query Match 100.0%; Score 22; DB 13; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4  
 Db 50 DRVY 53

RESULT 9  
 Q08555 PRELIMINARY; PRT; 57 AA.  
 AC Q08555;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE QUAIL DNA FOR TYROSINE KINASE RECEPTOR (PDGFR/FMS) (CLONE CK1)  
 DE (FRAGMENT).  
 OS Phasianidae.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes.

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OX NCBI_TaxID=9005;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93096482; PubMed=1281306;
RA Marcelle C., Eichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RL the avian embryo.";
RL Oncogene 7:2479-2487(1992).
DR EMBL; X69694; CAA49364.1; -.
DR InterPro; IPR000719; Euk.pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Receptor; Transferase.
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6586 MW; AB0689E2ED7B58ED CRC64;

Query Match 100.0%; Score 22; DB 13; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4
DB 50 DRVY 53

RESULT 10
Q9LJ70
ID Q9LJ70 PRELIMINARY; PRT; 61 AA.
AC Q9LJ70;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILARITY TO LYSYL-TRNA SYNTHETASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000411; BAB02142.1; -.
DR HSSP; P14825; 1LYL.
DR InterPro; IPR004364; tRNA-synt_2.
DR InterPro; IPR002313; tRNA-synt_lys_2.
DR Pfam; PF00152; tRNA-synt_2; 1.
DR PRINTS; PR00982; TRNASYNTHLYS.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 61 AA; 7075 MW; A8E725C053AFB2C4 CRC64;

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Query Match 100.0%; Score 22; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4
DB 44 DRVY 47

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RESULT 11
Q9NPE3
ID Q9NPE3 PRELIMINARY; PRT; 64 AA.
AC Q9NPE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NOP10P (NUCLEOLAR PROTEIN FAMILY A, MEMBER 3) (H/ACA SMALL NUCLEOLAR
DE RNPS).
GN NOP10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP Toji S., Yano M., Tamai K.;
RT "Human Nop10p cDNA.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99059744; PubMed=9843512;
RA Henras A., Henry Y., Bousquet-Antonelli C., Noaillac-Depeyre J.,
RA Gelugne J., Caizergues-Ferrer M.;
RT "Nhp2p and Nop10p are essential for the function of H/ACA snRNPs.";
RL EMBO J. 17:7078-7090(1998).
RN [3]
RN SEQUENCE FROM N.A.
RP Toji S., Yano M., Tamai K.;
RT "Human Nop10p genomic DNA.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB043104; BAA96133.1; -.
DR EMBL; AB043103; BAA96107.1; -.
DR EMBL; BC008886; AAH08886.1; -.
SQ SEQUENCE 64 AA; 7706 MW; 62E9BCFFB27036FA CRC64;

Query Match 100.0%; Score 22; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4
DB 12 DRVY 15

RESULT 12
Q9V5P6
ID Q9V5P6 PRELIMINARY; PRT; 64 AA.
AC Q9V5P6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG7637 PROTEIN.
GN CG7637.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle K., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.P., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RT Science 287:2185-2195(2000).  
 DR EMBL: AE003828; AAF58753.1; -;  
 DR FLYbase: FBgn0033548; CG7637.  
 SQ SEQUENCE 64 AA; 7634 MW; B957575884DEA7CF CRC64;

Query Match 100.0%; Score 22; DB 5; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
 Db 12 DRVY 15

RESULT 13

ID O9CQS2 PRELIMINARY; PRT; 64 AA.  
 AC O9CQS2;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE 1110036B12RIK PROTEIN.  
 GS 1110036B12RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guscincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombearts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK012875; BAB28529.1; -;  
 DR EMBL: AK004120; BAB23180.1; -;  
 DR MGD: MGI:1913431; 1110036B12RIK.  
 SQ SEQUENCE 64 AA; 7706 MW; 62E9BCFFB27036FA CRC64;

Query Match 100.0%; Score 22; DB 11; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
 Db 12 DRVY 15

RESULT 14

ID O76159 PRELIMINARY; PRT; 66 AA.  
 AC O76159;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE RECEPTOR TYROSINE KINASE (FRAGMENT).  
 OS Dugesia japonica (Planarian).  
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;  
 OC Paludicola; Dugesidae; Dugesia.  
 OC NCBI\_TaxID=6161;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GI;  
 RX MEDLINE=98340876; PubMed=9675112;  
 RA Ogawa K., Wakayama A., Kunisada T., Orii H., Watanabe K., Agata K.;  
 RT "Identification of a receptor tyrosine kinase involved in germ cell  
 RT differentiation in planarians.";  
 RL Biochem. Biophys. Res. Commun. 248:204-209(1998).  
 DR EMBL: AB014498; BAA32049.1; -;  
 DR HSP; P11362; IFGK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Kinase; Transferase.  
 FT NON\_TER 1  
 FT NON\_TER 66  
 SQ SEQUENCE 66 AA; 7709 MW; 09D367D0E95F04B2 CRC64;

Query Match 100.0%; Score 22; DB 5; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
 Db 53 DRVY 56

RESULT 15

ID Q90957 PRELIMINARY; PRT; 67 AA.  
 AC Q90957;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

Mon Jul 1 10:44:29 2002

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PROTEIN-TYROSINE KINASE (FRAGMENT).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LENS;  
RA Potts J.D., Harocopos G.J., Beebe D.C.;  
RT "Identification of receptor tyrosine kinases in the embryonic chicken  
lens.";  
RL Curr. Eye Res. 0:0-0(1993).  
DR EMBL; L20623; AAA49043.1; -.  
DR HSP; P11362; IFGK.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Kinase; Transferase.  
FT NON\_TER 1  
FT NON\_TER 67  
SQ SEQUENCE 67 AA; 7856 MW; F6EFB106477A9AB1 CRC64;

Query Match 100.0%; Score 22; DB 13; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVY 4  
DB 55 DRVY 58

Search completed: July 1, 2002, 07:45:16  
Job time: 412 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: July 1, 2002, 07:41:55 ; Search time 158.26 Seconds  
(without alignments)  
2.106 Million cell updates/sec

Title: US-09-723-197-11  
Sequence: 1 DRV 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	3	19	AAW64738
2	15	100.0	3	19	AAW71120
3	15	100.0	3	20	AAW30549
4	15	100.0	3	20	AAW30593
5	15	100.0	3	21	AAW84134
6	15	100.0	4	17	AAW95671
7	15	100.0	4	19	AAW64737
8	15	100.0	4	19	AAW65606
9	15	100.0	4	19	AAW71119
10	15	100.0	4	19	AAW61302
11	15	100.0	4	19	AAW61138

12	15	100.0	4	19	AAW47218	Variant MHC Class
13	15	100.0	4	20	AAW49595	Angiotensin analog
14	15	100.0	4	20	AAW33910	Angiotensin II ana
15	15	100.0	4	20	AAW30548	Amino acid sequenc
16	15	100.0	4	20	AAW30592	Angiotensin II ana
17	15	100.0	4	20	AAW32723	Angiotensin II ana
18	15	100.0	4	20	AAW33777	Angiotensin II (AI
19	15	100.0	4	20	AAW15354	Angiotensin II (AI
20	15	100.0	4	20	AAW15314	Angiotensin II (AI
21	15	100.0	4	21	AAW27410	Angiotensin II ana
22	15	100.0	4	21	AAW28108	Angiotensin II ana
23	15	100.0	4	21	AAW84133	Peptide comprising
24	15	100.0	4	21	AAW77046	Angiotensin II (AI
25	15	100.0	4	21	AAW57410	Angiotensin peptid
26	15	100.0	4	22	AAE08880	Angiotensin peptid
27	15	100.0	4	22	AAE02997	Human angiotensin
28	15	100.0	4	22	AAE03160	Human angiotensin
29	15	100.0	4	22	AAW91467	Angiotensin peptid
30	15	100.0	5	8	AAW71638	Diuretic peptide d
31	15	100.0	5	11	AAW09372	Sequence of atrial
32	15	100.0	5	14	AAW65519	Endothelin antag
33	15	100.0	5	17	AAW95670	Angiotensin II fra
34	15	100.0	5	18	AAW31079	Mugwort pollen all
35	15	100.0	5	19	AAW64736	Angiotensin II pep
36	15	100.0	5	19	AAW65605	Angiotensin II ana
37	15	100.0	5	19	AAW71118	Peptide AII(1-5) u
38	15	100.0	5	19	AAW75554	M. tuberculosis 80
39	15	100.0	5	19	AAW37888	Mycobacterium tube
40	15	100.0	5	20	AAW49594	Angiotensin analog
41	15	100.0	5	20	AAW33909	Angiotensin II' ana
42	15	100.0	5	20	AAW30547	Amino acid sequenc
43	15	100.0	5	20	AAW30591	Amino acid sequenc
44	15	100.0	5	20	AAW32722	Angiotensin II ana
45	15	100.0	5	20	AAW33776	Angiotensin II (AI

ALIGNMENTS

RESULT 1

AAW64738

ID AAW64738 standard; peptide; 3 AA.

XX AC AAW64738;

XX DT 02-NOV-1998 (first entry)

XX DE Angiotensin II peptide #10.

XX KW Proliferation; mesenchymal stem cell; lineage-specific cell;

XX KW haematopoietic; cell culture; transplantation; treatment; malignant;

XX KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9832457-A2.

XX PD 30-JUL-1998.

XX PF 26-JAN-1998; 98WO-US01552.

XX PR 23-JAN-1998; 98US-0066593.

XX PR 28-JAN-1997; 97US-0036507.

XX PR 08-MAY-1997; 97US-0046859.

XX PR 28-OCT-1997; 97US-0063684.

XX PR 31-OCT-1997; 97US-0063910.

XX PR 18-NOV-1997; 97US-0065612.

XX PR 26-NOV-1997; 97US-0066593.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX XX diZerega G, Rodgers KE;

XX WPI; 1998-437044/37.  
 XX  
 XX Promoting haematopoietic and mesenchymal cell proliferation and  
 PT differentiation - by contacting the cells with angiotensinogen,  
 PT angiotensin I or II, or analogues or fragments of these  
 XX  
 XX Claim 7; Page 14; 114pp; English.  
 XX  
 XX AAW64728-W64763 are peptides used in a novel method for accelerating the  
 CC proliferation of mesenchymal stem cells (MSCs), haematopoietic  
 CC lineage-specific cells or mesenchymal lineage-specific cells. The method  
 CC involves contacting the cells with an active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R1-R8 in  
 CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8, R1 and R2 together  
 CC form a group of formula X-Ra-Rb, X = H or a 1-3 peptide group, R3 = Val,  
 CC Ala, Leu, norleu, Ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane  
 CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or  
 CC azATyr, R5 = Ile, Ala, Leu, norleu, Val or Gly; R6 = His, Arg or  
 CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are  
 CC not defined in the specification, the peptide bond between Ra and Rb is  
 CC labile to aminopeptidase A cleavage excluding sequences including R4 as a  
 CC terminal Tyr group. A second active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R2-R8 in  
 CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,  
 CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also  
 CC described. The inventions are particularly useful in cell culture  
 CC mediums. These cells may be used in transplantation techniques for  
 CC treatment of malignant or inherited diseases. The formulae represent  
 CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),  
 CC or AII AT2 type 2 receptor agonists.  
 XX  
 XX Sequence 3 AA;

Query Match 100.0%; Score 15; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 Db 1 drv 3

## RESULT 2

AAW71120  
 ID AAW71120 standard; peptide; 3 AA.

XX  
 AC AAW71120;

XX 27-OCT-1998 (first entry)

XX Peptide AII(1-3) used to accelerate thermal wound healing.

XX Angiotensin; AII; acceleration; thermal wound healing; human;  
 KW growth factor release; neovascularisation; re-epithelialisation;  
 KW extracellular matrix production.

XX Synthetic.

XX WO9833813-A2.

XX 06-AUG-1998.

XX 04-FEB-1998; 98WO-US02049.

XX 04-FEB-1997; 97US-0037166.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1998-437391/37.

XX Methods for accelerating thermal wound healing in humans - using  
 PT angiotensinogen II and AII analogues  
 XX  
 XX Claim 3; Page 9; 58pp; English.

XX AAW71110-27 represent peptide used in the method of the invention. The  
 CC specification describes a method of accelerating thermal wound healing  
 CC in humans. The method comprises applying to the thermally injured tissue  
 CC an amount of at least one active agent which comprises the peptides  
 CC AAW71115-27. The method can be used to promote the healing of thermal  
 CC wounds by accelerating growth factor release, neovascularisation,  
 CC re-epithelialisation and extracellular matrix production. The sequences  
 CC are analogues of the angiotensin or angiotensinogen family of proteins.

XX Sequence 3 AA;

Query Match 100.0%; Score 15; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 Db 1 drv 3

## RESULT 3

AAV30549  
 ID AAV30549 standard; peptide; 3 AA.

XX  
 AC AAV30549;

XX 18-NOV-1999 (first entry)

XX Amino acid sequence of angiotensin II fragment AIII-3.

XX Angiotensin; analogue; tissue equivalent; cell proliferation.

XX Synthetic.

XX WO9946285-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-US05261.

XX 11-MAR-1998; 98US-0077499.

XX 12-JUN-1998; 98US-0089064.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-551360/46.

XX An improved method for producing a tissue equivalent with angiotensin I  
 PT and II derived active agents -

XX Claim 2; Page 10; 83pp; English.

XX AAV30539-80 represent angiotensin I (AI) and angiotensin (II), AII  
 CC fragments and AII analogues. The peptides are used in the method  
 CC of the invention. The specification describes an improved method  
 CC for producing a tissue equivalent. The method comprises contacting  
 CC the tissue equivalent with angiotensin I and II derived active  
 CC agents. The methods are used for production and culture of tissue  
 CC equivalents (three-dimensional cell and tissue culture systems),  
 CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,  
 CC vascular graft, cartilage, ligament, collagen lattice, liver and  
 CC kidney tissue equivalents. The methods and tissue culture systems  
 CC are used for the long-term proliferation of cells and tissues  
 CC in an in vitro environment that more closely approximates that found

CC In vivo.  
XX  
SQ Sequence 3 AA;

Query Match 100.0%; Score 15; DB 20; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DRV 3  
|||  
Db 1 drv 3

RESULT 4  
AAY30593  
ID AAY30593 standard; peptide; 3 AA.  
XX  
AC AAY30593;  
XX  
DT 18-NOV-1999 (first entry)  
XX  
DE Amino acid sequence of an angiotensin II (AII) fragment AII1-3.  
XX

KW Angiotensin; analogue; radiation mitigation; tissue damage;  
KW radiation therapy; bone marrow transplantation;  
KW megakaryocyte production; platelet production; cancer therapy;  
KW gene therapy; hematopoietic disorder.  
XX  
OS Synthetic.  
XX  
PN WO9945945-A1.  
XX  
PD 16-SEP-1999.  
XX  
PF 08-MAR-1999; 99WO-0505194.  
XX  
PR 10-MAR-1998; 98US-0077382.  
PR 09-APR-1998; 98US-0081262.  
PR 30-APR-1998; 98US-0083670.  
PR 19-JUN-1998; 98US-0090096.  
PR 22-JUN-1998; 98US-0090216.  
PR 11-SEP-1998; 98US-0099957.  
XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
PA (RODS/) RODGERS K E.  
PA (DIZE/) DIZEREGA G.  
XX  
PI Rodgers KE, Dizerega G;  
XX  
WPI; 1999-551209/46.  
XX

Use of angiotensin and angiotensin type peptides, for mitigating  
PT radiation induced tissue damage, improving bone marrow transplantation  
PT and promoting megakaryocyte and platelet production  
XX  
PS Claim 2; Page 90; 116pp; English.  
XX  
CC AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII  
CC fragments and AII analogues. The peptides are used in the method  
CC of the invention. The specification describes a method for mitigating  
CC radiation induced tissue damage, improving the effectiveness of  
CC radiation therapy, to support bone marrow transplantation, and  
CC promoting megakaryocyte production and mobilization and platelet  
CC production. The method comprises administration of the present peptides.  
CC The methods can be used to mitigate radiation induced tissue damage, to  
CC improve the effectiveness of radiation therapy, to support bone marrow  
CC transplantation, and to promote megakaryocyte production and  
CC mobilization and platelet production. They are used particularly in  
CC cancer therapy. They can also be used to provide megakaryocytes as  
CC vehicles for gene therapy in hematopoietic disorders, by providing a  
CC more efficient means to rapidly expand transduced megakaryocytes.  
XX

SQ Sequence 3 AA;

Query Match 100.0%; Score 15; DB 20; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DRV 3  
|||  
Db 1 drv 3

RESULT 5  
AAY84134  
ID AAY84134 standard; peptide; 3 AA.  
XX  
AC AAY84134;  
XX  
DT 03-JUL-2000 (first entry)  
XX  
DE Peptide comprising amino acids 1-3 of angiotensin II.  
XX

KW Angiotensin III; angiotensinogen; angiotensin I; angiotensin II;  
KW analogue; blood flow; ischemic tissue; angiogenesis; cardiac remodelling;  
KW congestive heart disease; ischemic myocardial infarction;  
KW embryonic development; wound healing; chronic inflammatory disease.  
XX  
OS Synthetic.  
XX  
PN WO200009144-A1.  
XX  
PD 24-FEB-2000.  
XX  
PF 12-AUG-1999; 99WO-US18374.  
XX  
PR 13-AUG-1998; 98US-0096414.  
PR 18-SEP-1998; 98US-0101024.  
XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX  
PI Rodgers K, Dizerega G;  
XX  
WPI; 2000-237409/20.  
XX

Increasing blood flow to ischemic tissue for minimizing cardiac  
PT remodelling and development of congestive heart failure involves  
PT administration of an active agent  
XX  
PS Claim 2; Page 43; 56pp; English.  
XX  
CC The present sequence represents an angiotensin II fragment. The  
CC specification also describes peptides derived from angiotensinogen,  
CC angiotensin I, angiotensin II, angiotensin III, and their analogues.  
CC The peptides are used for increasing blood flow to ischemic tissue.  
CC The peptides are angiotensin stimulators. The peptides are useful for  
CC increasing blood flow to ischemic tissue by stimulating angiogenesis,  
CC and minimizing cardiac remodelling and development of congestive heart  
CC disease following a ischemic myocardial infarction. The stimulation of  
CC angiogenesis is also useful for embryonic development, wound healing  
CC and treating chronic inflammatory disease.  
XX

SQ Sequence 3 AA;

Query Match 100.0%; Score 15; DB 21; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DRV 3  
|||  
Db 1 drv 3

RESULT 6  
 AAR95671  
 ID AAR95671 standard; peptide; 4 AA.  
 XX  
 AC AAR95671;  
 XX  
 DT 09-JAN-1997 (first entry)  
 XX  
 DE Angiotensin II fragment AII(1-4).  
 XX  
 KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;  
 KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;  
 KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9614858-A1.  
 XX  
 PD 23-MAY-1996.  
 XX  
 PF 14-NOV-1995; 95WO-US14764.  
 XX  
 PR 06-JUN-1995; 95US-0465775.  
 PR 14-NOV-1994; 94US-0337781.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Dizerega GS, Rodgers K;  
 XX  
 DR WPI; 1996-259561/26.  
 XX  
 PT Accelerating wound healing by application of angiotensin II  
 PT fragments - are effective at very low concn. and do not cause  
 PT hypertension  
 XX  
 PS Disclosure; Page 4; 46pp; English.  
 XX  
 CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see  
 CC AAR95662) is an octapeptide present in humans and other species. AT2 is  
 CC one of the most potent vasoconstrictors known, causing constriction of  
 CC the arterioles. The formation of angiotensin is initiated by the action  
 CC of renin on angiotensinogen. The substance formed is a decapeptide  
 CC called angiotensin I which is converted by the enzyme angiotensinase (by  
 CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release  
 CC of extracellular matrices involved in wound repair. These fragments can  
 CC be used in a compound for accelerating wound healing. The compounds are  
 CC administered as matricial or micellar solutions, formulated with a  
 CC carrier or diluent, alternatively the compound is applied in conjuncture  
 CC with a wound dressing. The carrier used in the composition is  
 CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly  
 CC glycols. By using fragments of this sequence (or analogues of it),  
 CC growth as well as healing of tissues is improved, such as in cases of  
 CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or  
 CC intraperitoneal surgical wounds. The compounds containing the AT2  
 CC fragments are less hypertensive than full length AT2, and are also  
 CC effective at much lower (nanomolar) concentrations than full length AT2.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 15; DB 17; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRV 3  
 DB 1 drv 3  
 RESULT 7  
 AAR64737  
 ID AAR64737 standard; peptide; 4 AA.  
 XX

AC AAW64737;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE Angiotensin II peptide #9.  
 XX  
 KW Proliferation; mesenchymal stem cell; lineage-specific cell;  
 KW haematopoietic; cell culture; transplantation; treatment; malignant;  
 KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9832457-A2.  
 XX  
 PD 30-JUL-1998.  
 XX  
 PF 26-JAN-1998; 98WO-US01552.  
 XX  
 PR 23-JAN-1998; 98US-0066593.  
 PR 28-JAN-1997; 97US-0036507.  
 PR 08-MAY-1997; 97US-0046859.  
 PR 28-OCT-1997; 97US-0063684.  
 PR 31-OCT-1997; 97US-0063910.  
 PR 18-NOV-1997; 97US-0065612.  
 PR 26-NOV-1997; 97US-0066593.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Dizerega G, Rodgers KE;  
 XX  
 DR WPI; 1998-437044/37.  
 XX  
 PT Promoting haematopoietic and mesenchymal cell proliferation and  
 PT differentiation - by contacting the cells with angiotensinogen,  
 PT angiotensin I or II, or analogues or fragments of these  
 XX  
 PS Claim 7; Page 14; 114pp; English.  
 XX  
 CC AAW64728-W64763 are peptides used in a novel method for accelerating the  
 CC proliferation of mesenchymal stem cells (MSCs), haematopoietic  
 CC lineage-specific cells or mesenchymal lineage-specific cells. The method  
 CC involves contacting the cells with an active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R1-R8 in  
 CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together  
 CC form a group of formula X-Ra-Rb- X = H or a 1-3 peptide group, R3 = Val,  
 CC Ala, Leu, norleu, Ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane  
 CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoser or  
 CC azatyr, R5 = Ile, Ala, Leu, norleu, Val or Gly; R6 = His, Arg or  
 CC 6-NH2-Phe, R7 = pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are  
 CC not defined in the specification, the peptide bond between Ra and Rb is  
 CC labile to aminopeptidase A cleavage excluding sequences including R4 as a  
 CC terminal Tyr group. A second active agent comprising a sequence  
 CC consisting of at least three contiguous amino acids of groups R2-R8 in  
 CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,  
 CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also  
 CC described. The inventions are particularly useful in cell culture  
 CC mediums. These cells may be used in transplantation techniques for  
 CC treatment of malignant or inherited diseases. The formulae represent  
 CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),  
 CC or AII AT2 type 2 receptor agonists.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 15; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRV 3  
 DB 1 drv 3

RESULT 8  
 AAW65606  
 ID AAW65606 standard; peptide; 4 AA.  
 XX  
 AC AAW65606;  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Angiotensin II analogue, AII(1-4).  
 XX  
 KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;  
 KW wound healing.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9826795-A1.  
 XX  
 PD 25-JUN-1998.  
 XX  
 PF 16-DEC-1997; 97WO-US23461.  
 XX  
 PR 15-DEC-1997; 97US-0990664.  
 PR 16-DEC-1996; 96US-0028310.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Dizerega GS, Rodgers KE;  
 XX  
 DR WPI; 1998-362518/31.  
 XX  
 PT Promoting incorporation of skin graft onto underlying tissue -  
 PT comprises pre-treating graft with angiotensin II, or analogue or  
 PT peptide fragment  
 XX  
 PS Disclosure; Page 6; 82pp; English.  
 XX  
 CC The invention relates to the use of angiotensin II (AII), AII analogues,  
 CC AII fragments and AII fragment analogues for promoting incorporation of a  
 CC skin graft into underlying tissue of a mammal. The peptides are effective  
 CC in accelerating the growth or healing of skin grafts and in accelerating  
 CC re-epithelialisation and tissue repair, even at very low concentrations.  
 CC They can significantly accelerate the rate of healing at nanomolar levels  
 CC in vivo. AII accelerates wound repair by increased neovascularisation,  
 CC growth factor release, re-epithelialisation, extracellular matrix production  
 CC and increased flow of blood and nutrients to the injured tissue. Use of  
 CC the above peptides other than AII itself (an extremely potent vaso-  
 CC constrictor) may avoid the side-effects of AII, such as increase in blood  
 CC pressure and thirst. The present sequence represents an angiotensin  
 CC II fragment.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 15; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DRV 3  
 Db 1 drv 3  
 RESULT 9  
 AAW71119  
 ID AAW71119 standard; peptide; 4 AA.  
 XX  
 AC AAW71119;  
 XX  
 DT 27-OCT-1998 (first entry)  
 XX  
 DE Peptide AII(1-4) used to accelerate thermal wound healing.

XX Angiotensin; AII; acceleration; thermal wound healing; human;  
 KW growth factor release; neovascularisation; re-epithelialisation;  
 KW extracellular matrix production.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9833813-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 04-FEB-1998; 98WO-US02049.  
 XX  
 PR 04-FEB-1997; 97US-0037166.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Dizerega G, Rodgers KE;  
 XX  
 DR WPI; 1998-437391/37.  
 XX  
 PF Methods for accelerating thermal wound healing in humans - using  
 PT angiotensinogen II and AII analogues  
 XX  
 PS Claim 3; Page 9; 58pp; English.  
 XX  
 CC AAW71110-27 represent peptide used in the method of the invention. The  
 CC specification describes a method of accelerating thermal wound healing  
 CC in humans. The method comprises applying to the thermally injured tissue  
 CC an amount of at least one active agent which comprises the peptides  
 CC AAW71115-27. The method can be used to promote the healing of thermal  
 CC wounds by accelerating growth factor release, neovascularisation,  
 CC re-epithelialisation and extracellular matrix production. The sequences  
 CC are analogues of the angiotensin or angiotensinogen family of proteins.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 15; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DRV 3  
 Db 1 drv 3  
 RESULT 10  
 AAW61302  
 ID AAW61302 standard; peptide; 4 AA.  
 XX  
 AC AAW61302;  
 XX  
 DT 02-OCT-1998 (first entry)  
 XX  
 DE Peptide 17 used to generate antibody.  
 XX  
 KW Immunosuppression; immunodeficiency; viral infection; neoplastic tissue;  
 KW cytokine imbalance; hormone imbalance; myalgic encephalomyelitis; ME;  
 KW viral infection fatigue syndrome; tuberculosis infection;  
 KW malarial infection; post inoculation fatigue syndrome.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9810787-A2.  
 XX  
 PD 19-MAR-1998.  
 XX  
 PF 10-SEP-1997; 97WO-IB01086.  
 XX  
 PR 11-SEP-1996; 96US-0025180.  
 XX  
 PA (PREN/) PRENDERGAST P T.

XX Prendergast PT;  
 PI WPI; 1998-271637/24.  
 DR  
 XX Immune system directed therapy - using specific amino acid sequences  
 PT exhibiting ion bridge pair arrays enclosed by hydrophobic segments  
 XX  
 PS Claim 95; Page 76; 83pp; English.  
 XX  
 CC The immunosuppressive amino acid sequences AAW61280-W61314 are used in  
 CC the method of the invention to enhance immune response in a patient  
 CC suffering from: (a) immunodeficiency resultant from (i) a viral  
 CC infection; (ii) bacterial, mycoplasmic, fungal and/or parasitic  
 CC infections; (iii) the growth of neoplastic tissue; (iv) any cytokine or  
 CC hormone imbalance or imbalance of any natural product within the  
 CC patient; (b) myalgic encephalomyelitis (ME); (c) post inoculation or  
 CC viral infection fatigue syndrome; (d) tuberculosis infection, and (e)  
 CC malarial infection.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 15; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRV 3  
 DB |||  
 2 drv 4  
 RESULT 11  
 AAW61138  
 ID AAW61138 standard; peptide; 4 AA.  
 XX  
 AC AAW61138;  
 XX  
 DT 14-SEP-1998 (first entry)  
 XX  
 DE Peptide 17 used to produce antibodies against interleukin 10 mimc.  
 XX  
 KW Peptide; monoclonal; polyclonal; antibody; interleukin 10; IL10  
 KW alpha-fetoprotein; AFP; ion bridge pair array; infectious agent;  
 KW humoral; T cell; immune system; B cell; immunosuppression;  
 KW T helper cell; monocyte; cytotoxicity; IL2; gamma interferon; vaccine;  
 KW immunodeficiency; autoimmune disease; ss.  
 OS Synthetic.  
 XX  
 XX WO9810792-A1.  
 PN  
 XX  
 XX 19-MAR-1998.  
 PD  
 XX  
 XX 13-SEP-1996; 96WO-1B00945.  
 PF  
 XX  
 XX 11-SEP-1996; 96US-0025180.  
 PR  
 XX  
 XX (PREN/) PRENDERGAST P T.  
 PA  
 XX  
 XX Prendergast PT;  
 PI  
 XX WPI; 1998-260966/23.  
 DR  
 XX New immune system directed therapy - using specific amino acid  
 PT sequences which exhibit ion bridge pair arrays enclosed by a  
 PT non-polar hydrophobic segment  
 PT  
 XX  
 PS Claim 8; Page 25; 31pp; English.  
 XX  
 CC The peptides AAW61122-W61148 can be used to raise monoclonal or  
 CC polyclonal antibodies (Ab) against an interleukin 10 (IL-10) or  
 CC alpha-fetoprotein (AFP) mimic. The peptide sequences contain ion bridge

CC pair arrays which are utilised in the infectious agents to enhance the  
 CC humoral Ab response and down regulate the T cell or delayed-type  
 CC hypersensitivity response. The peptides identified are used by infectious  
 CC agents to undermine the host's immune defence system and also to gain  
 CC entry to the target lymphoid tissue. This is caused by the non-specific  
 CC polyclonal B cell activation and immunosuppression. The mimic molecules  
 CC shut down the required Th1 T cell response which is needed to clear the  
 CC intracellular infections. Due to this, not enough immune reactive  
 CC monocytes are produced to overcome the initial infection. Upon  
 CC administration of the Ab, there will be an immediate Ab-dependent,  
 CC cell-mediated cytotoxicity-stimulated reduction in viral load, due to the  
 CC reduction of the IL-10/AFP mimic. Due to the presence of the Ab in the  
 CC hosts, the IL-10 and AFP mimics are no longer invisible and the Th1  
 CC response can be initiated, causing the synthesis of IL-2 and  
 CC gamma-interferon. The peptides can be used in the production of a  
 CC vaccine for the treatment of immunodeficiency, autoimmune disease,  
 CC infections, immune system disorders, etc.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 15; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRV 3  
 DB |||  
 2 drv 4  
 RESULT 12  
 AAW47218  
 ID AAW47218 standard; peptide; 4 AA.  
 XX  
 AC AAW47218;  
 XX  
 DT 26-JUN-1998 (first entry)  
 XX  
 DE Variant MHC Class II DR beta-chain beta 1 domain residues 75-78.  
 XX  
 KW Determination; susceptibility; resistance; bovine leukaemia;  
 KW bovine leukaemia virus; BLV; beta 1 domain; bovine; MHC Class II;  
 KW DR beta-chain.  
 XX  
 OS Bos taurus.  
 XX  
 XX WO9803680-A1.  
 PN  
 XX  
 XX 29-JAN-1998.  
 PD  
 XX  
 XX 17-JUL-1997; 97WO-JP02485.  
 PF  
 XX  
 XX 28-MAR-1997; 97JP-0077979.  
 PR  
 XX 19-JUL-1996; 96JP-0190933.  
 PR  
 XX (RIKA ) INST PHYSICAL & CHEM RES.  
 PA  
 XX  
 XX Aida Y;  
 PI  
 XX WPI; 1998-120797/11.  
 DR  
 XX  
 XX Detecting susceptibility or resistance to bovine leukaemia caused by  
 PT bovine leukaemia virus - by detecting specific residues of the beta  
 PT 1 domain of bovine MHC Class II DR-beta chain; useful in cattle  
 PT farming  
 PT  
 XX Example 1; Page 11; 28pp; Japanese.  
 PS  
 XX The present sequence was used in the development of a novel method  
 CC to determine susceptibility, or resistance to bovine leukaemia  
 CC caused by bovine leukaemia virus (BLV). The method comprises  
 CC amplifying DNA encoding all or part of the beta 1 domain of the  
 CC bovine MHC Class II DR beta-chain from bovine genomic DNA,



CC expressing the DNA to give a beta 1 domain product and detecting  
 CC the amino acid sequence AAW47215, which is indicative of  
 CC susceptibility to bovine leukaemia caused by BLV, or Val78 in the  
 CC beta 1 domain which is indicative of resistance to bovine leukaemia  
 CC caused by BLV. Determination of the susceptibility or resistance to  
 CC bovine leukaemia caused by BLV is useful in dairy farming breeding  
 CC programs.

XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 15; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 DB 2 drv 4

RESULT 13  
 AAY49595  
 ID AAY49595 standard; peptide; 4 AA.

XX AC AAY49595;

XX DT 13-JAN-2000 (first entry)

XX DE Angiotensin analogue peptide SEQ ID NO:10.

XX KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;  
 KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.  
 XX OS Synthetic.

XX PN WO9952540-A1.

XX PD 21-OCT-1999.

XX PF 07-APR-1999; 99WO-US07654.

XX PR 09-APR-1998; 98US-0081262.

XX PR 12-JUN-1998; 98US-0089024.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers KE, Dizerega G;

XX PS WPI; 1999-620285/53.

XX PT Treating or preventing infections in mammals using peptides derived  
 PT from angiotensin or angiotensin receptor agonists

XX Claim 2; Page 10; 91pp; English.

XX The present invention describes a method for treating or preventing  
 CC infections in mammals by administering peptides (A) that are fragments  
 CC or analogues (or their fragments) of angiotensinogen, angiotensins I or  
 CC II, or angiotensin II AT<sub>2</sub>-type receptor agonists. (A) contain at least  
 CC 3 consecutive amino acids (aa) from the sequence (S1):  
 CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = x-Ra-Rb-;  
 CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane  
 CC carboxylic acid), Ala, dimethylglycine, pro, betaine, Glu(NH<sub>2</sub>), Gly,  
 CC Asp(NH<sub>2</sub>) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,  
 CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,  
 CC Ile, Gly, Pro, Alb (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr  
 CC (optionally phosphorylated), Thr, Ser, homoserine, pro, Ala or aza-Tyr;  
 CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;  
 CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =  
 CC sequences having R4 as a terminal Tyr residue are excluded. The method  
 CC is particularly used in cases of bacterial infection (e.g. septic shock,  
 CC peritonitis, bacteraemia or endotoxaemia) but also against viral and  
 CC parasitic infections. AAY49586 to AAY49623 represent specifically

CC claimed examples of (A).  
 XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 15; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 DB 1 drv 3

RESULT 14  
 AAY33910

ID AAY33910 standard; peptide; 4 AA.

XX AC AAY33910;

XX DT 29-NOV-1999 (first entry)

XX DE Angiotensin II analogue AII(1-4).

XX KW embryonic stem cell; ES; angiotensin; totipotent cell;  
 KW gene therapy; replacement therapy; angiotensin II; AII;  
 KW analogue.

XX OS Homo sapiens.

XX PN WO9942122-A1.

XX PD 26-AUG-1999.

XX PF 16-FEB-1999; 99WO-US03243.

XX PR 19-FEB-1998; 98US-0075179.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX PS WPI; 1999-527419/44.

XX PT Promoting embryonal cell proliferation, using angiotensinogen and  
 PT angiotensin peptides, analogs or fragments

XX Claim 2; Page 8; 76pp; English.

XX This is the amino acid sequence of the Angiotensin II analogue,  
 CC AII(1-4). The formation of Angiotensin II (AII) is initiated by the  
 CC action of renin on the plasma substrate angiotensinogen.  
 CC This results in Angiotensin I (AI) which then converted to AII by the  
 CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
 CC residues from AI (AAY42372).  
 CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and  
 CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,  
 CC or AII AT<sub>2</sub> type 2 receptor agonists can rapidly provide a large  
 CC population of ESCs (Embryonic Stem Cell) for use in replacement therapy.  
 CC Similarly, methods that increase in vivo proliferation of ESCs will  
 CC enhance the utility of replacement therapy by rapidly increasing local  
 CC concentration of the stem cells and their progeny at the site of  
 CC therapy. The method also increases the potential utility of ESCs as  
 CC vehicles for gene therapy in certain disorders by more efficiently  
 CC providing a large number of such cells for transfection, and also by  
 CC providing a more efficient means to rapidly expand transfected ESCs.

XX Sequence 4 AA;

Query Match 100.0%; Score 15; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 drv 3

RESULT 15

AAAY30548  
ID AAAY30548 standard; peptide; 4 AA.

AC AAAY30548;

XX 18-NOV-1999 (first entry)

XX Amino acid sequence of angiotensin II fragment AII1-4.

XX Angiotensin; analogue; tissue equivalent; cell proliferation.

XX Synthetic.

XX WO9946285-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-US05261.

XX 11-MAR-1998; 98US-0077499.

XX 12-JUN-1998; 98US-0089064.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-551360/46.

PT An improved method for producing a tissue equivalent with angiotensin I

PS Claim 2; Page 57; 83pp; English.

CC AAAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII  
fragments and AII analogues. The peptides are used in the method  
of the invention. The specification describes an improved method  
for producing a tissue equivalent. The method comprises contacting  
the tissue equivalent with angiotensin I and II derived active  
agents. The methods are used for production and culture of tissue  
equivalents (three-dimensional cell and tissue culture systems),  
chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,  
vascular graft, cartilage, ligament, collagen lattice, liver and  
kidney tissue equivalents. The methods and tissue culture systems  
are used for the long-term proliferation of cells and tissues  
in an in vitro environment that more closely approximates that found  
in vivo.

XX Sequence 4 AA;

Query Match 100.0%; Score 15; DB 20; Length 4;  
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 drv 3

Search completed: July 1, 2002, 07:41:56  
Job time: 348 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:01 ; Search time 59.1 Seconds  
(without alignments)  
1.240 Million cell updates/sec

Title: US-09-723-197-11  
Perfect score: 15  
Sequence: 1 DRV 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	3	2	US-08-465-775-11
2	15	100.0	3	3	US-09-208-337-11
3	15	100.0	3	3	US-08-990-664-12
4	15	100.0	3	4	US-09-373-962-11
5	15	100.0	3	4	US-09-245-680-11
6	15	100.0	3	4	US-09-198-806C-11
7	15	100.0	3	4	US-09-352-191-11
8	15	100.0	3	4	US-09-012-400-11
9	15	100.0	4	2	US-08-465-775-10
10	15	100.0	4	3	US-09-147-550-113
11	15	100.0	4	3	US-09-208-337-10
12	15	100.0	4	3	US-08-990-664-11
13	15	100.0	4	4	US-09-373-962-10
14	15	100.0	4	4	US-09-245-680-10
15	15	100.0	4	4	US-09-198-806C-10
16	15	100.0	4	4	US-09-352-191-10
17	15	100.0	4	4	US-09-557-917-113
18	15	100.0	4	4	US-09-012-400-10
19	15	100.0	5	2	US-08-465-775-9
20	15	100.0	5	3	US-09-109-063-60
21	15	100.0	5	3	US-08-724-814-2
22	15	100.0	5	3	US-09-208-337-9
23	15	100.0	5	3	US-08-990-664-10
24	15	100.0	5	4	US-09-373-962-9
25	15	100.0	5	4	US-09-245-680-9
26	15	100.0	5	4	US-09-198-806C-9
27	15	100.0	5	4	US-09-352-191-9

28	15	100.0	5	4	US-09-012-400-9	Sequence 9, Appli
29	15	100.0	5	5	PCT-US95-02373-2	Sequence 2, Appli
30	15	100.0	6	2	US-08-465-775-8	Sequence 8, Appli
31	15	100.0	6	3	US-09-208-337-8	Sequence 8, Appli
32	15	100.0	6	3	US-08-990-664-9	Sequence 9, Appli
33	15	100.0	6	4	US-09-373-962-8	Sequence 8, Appli
34	15	100.0	6	4	US-09-245-680-8	Sequence 8, Appli
35	15	100.0	6	4	US-09-198-806C-8	Sequence 8, Appli
36	15	100.0	6	4	US-09-352-191-8	Sequence 8, Appli
37	15	100.0	6	4	US-09-012-400-8	Sequence 8, Appli
38	15	100.0	7	1	US-07-803-623B-16	Sequence 16, Appli
39	15	100.0	7	2	US-08-806-084-16	Sequence 16, Appli
40	15	100.0	7	2	US-08-465-775-4	Sequence 4, Appli
41	15	100.0	7	2	US-09-047-594-1	Sequence 1, Appli
42	15	100.0	7	3	US-09-208-337-4	Sequence 4, Appli
43	15	100.0	7	3	US-08-990-664-5	Sequence 5, Appli
44	15	100.0	7	4	US-09-371-710-19	Sequence 19, Appli
45	15	100.0	7	4	US-09-373-962-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-465-775-11  
; Sequence 11, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-775-11

Query Match 100.0%; Score 15; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3

Db 1 DRV 3

RESULT 2  
US-09-208-337-11  
; Sequence 11, Application US/09208337  
; Patent No. 6096709  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: Gere, dizerega  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,337  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/465,775  
; APPLICATION NUMBER: 08/465,775  
; FILING DATE: 06-JUN-1995  
; APPLICATION NUMBER: 08/337,781  
; FILING DATE: 14-NOV-1994  
; APPLICATION NUMBER: 08/136,368  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC010.001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 949-760-0404  
; TELEFAX: 949-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-09-208-337-11

Query Match 100.0%; Score 15; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 3  
US-08-990-664-12  
; Sequence 12, Application US/08990664  
; Patent No. 6110895  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
; TITLE OF INVENTION: IN SKIN GRAFTS  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/990,664  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 60/028,310  
; APPLICATION NUMBER: 60/028,310  
; FILING DATE: 16-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC012.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-760-0404  
; TELEFAX: 714-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-990-664-12

Query Match 100.0%; Score 15; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 4  
US-09-373-962-11  
; Sequence 11, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ALI (1-3)  
US-09-373-962-11

Query Match 100.0%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 5  
US-09-245-680-11  
; Sequence 11, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245.680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-3)  
US-09-245-680-11

Query Match 100.0%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 6  
US-09-198-806C-11  
; Sequence 11, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198.806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-3)  
US-09-198-806C-11

Query Match 100.0%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 7  
US-09-352-191-11  
; Sequence 11, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue

; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352.191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-3)  
US-09-352-191-11

Query Match 100.0%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 8  
US-09-012-400-11  
; Sequence 11, Application US/09012400D  
; Patent No. 6335195  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell  
; TITLE OF INVENTION: Proliferation and Differentiation  
; FILE REFERENCE: 97,017-G  
; CURRENT APPLICATION NUMBER: US/09/012.400D  
; CURRENT FILING DATE: 1998-01-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-3)  
US-09-012-400-11

Query Match 100.0%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 9  
US-08-465-775-10  
; Sequence 10, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: PatentIn  
FILING DATE: 08/08/95  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-360  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-775-10

Query Match 100.0%; Score 15; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
DB 1 DRV 3

RESULT 10  
US-09-147-550-113  
Sequence 113, Application US/09147550  
Patent No. 6090540  
GENERAL INFORMATION:  
APPLICANT: Alda, Yoko  
TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF  
FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550  
CURRENT APPLICATION NUMBER: US/09/147,550  
CURRENT FILING DATE: 1999-04-23  
EARLIER APPLICATION NUMBER: PCT/JP97/02485  
EARLIER FILING DATE: 1997-07-17  
EARLIER APPLICATION NUMBER: JP 8-190933  
EARLIER FILING DATE: 1996-07-19  
EARLIER APPLICATION NUMBER: JP 9-77979  
EARLIER FILING DATE: 1997-03-28  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 113  
LENGTH: 4  
TYPE: PRT  
ORGANISM: BOVINE  
US-09-147-550-113

Query Match 100.0%; Score 15; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
DB 2 DRV 4

RESULT 11  
US-09-208-337-10  
Sequence 10, Application US/09208337  
Patent No. 6096709

GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: Gere, dizerega  
TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICANT: PatentIn  
FILING DATE: 08/09/95  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,775  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: 08/337,781  
FILING DATE: 14-NOV-1994  
APPLICATION NUMBER: 08/126,368  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: USC010.001CP2  
TELEPHONE: 949-760-0404  
TELEFAX: 949-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-208-337-10

Query Match 100.0%; Score 15; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
DB 1 DRV 3

RESULT 12  
US-08-990-664-11  
Sequence 11, Application US/08990664  
Patent No. 6110895  
GENERAL INFORMATION:  
APPLICANT: Rodgers, Kathleen  
APPLICANT: dizerega, Gere  
TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
TITLE OF INVENTION: IN SKIN GRAFTS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/990,664  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/028,310  
FILING DATE: 16-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: USC012.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-990-664-11

Query Match 100.0%; Score 15; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 13  
US-09-373-962-10  
; Sequence 10, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: diZerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)  
US-09-373-962-10

Query Match 100.0%; Score 15; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 14  
US-09-245-680-10  
; Sequence 10, Application US/09245680B

; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: diZerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245,680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)  
US-09-245-680-10

Query Match 100.0%; Score 15; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 15  
US-09-198-806C-10  
; Sequence 10, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: diZerega, Gere  
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-4)  
US-09-198-806C-10

Query Match 100.0%; Score 15; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

Search completed: July 1, 2002, 07:43:01  
Job time: 302 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:31 ; Search time 69.93 Seconds  
(without alignments)  
4.122 Million cell updates/sec

Title: US-09-723-197-11  
Perfect score: 15  
Sequence: 1 DRV 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	10	2	A60624	angiotensin I - Ja
2	15	100.0	10	2	S63432	angiotensin I - ho
3	15	100.0	10	2	A90917	angiotensin precu
4	15	100.0	10	2	A90345	angiotensin precu
5	15	100.0	14	2	A01250	angiotensin precu
6	15	100.0	15	2	A00834	angiotensin I prec
7	15	100.0	15	2	PA0041	plastoquinol-plas
8	15	100.0	18	2	H75063	hypothetical prote
9	15	100.0	20	2	A31049	calsequestrin, fas
10	15	100.0	20	2	A05313	apolipoprotein A-I
11	15	100.0	21	2	S03987	agglutinin beta-2
12	15	100.0	20	2	S03986	agglutinin beta-1
13	15	100.0	23	2	B39313	chaperonin, 10K -
14	15	100.0	23	2	C43732	NADH dehydrogenase
15	15	100.0	25	2	A60502	myonexin - norther
16	15	100.0	28	2	S57229	orotidine-5'-monop
17	15	100.0	33	2	A42592	precorrin-6x reduc
18	15	100.0	34	2	S68084	probable RNA-bindi
19	15	100.0	35	2	B84674	hypothetical prote
20	15	100.0	35	2	B82137	hypothetical prote
21	15	100.0	36	2	B82111	hypothetical prote
22	15	100.0	36	2	A61235	fibroblast-activat
23	15	100.0	36	2	A40723	poly-Ig receptor -
24	15	100.0	36	2	B82827	hypothetical prote
25	15	100.0	37	2	B85574	hypothetical prote
26	15	100.0	38	2	A60216	hyperglycemic horm
27	15	100.0	38	2	S78357	photosystem II pro
28	15	100.0	38	2	H82780	hypothetical prote
29	15	100.0	38	2	E89922	hypothetical prote

30	15	100.0	39	2	E69677	phosphatase (Rapi)
31	15	100.0	40	2	B27740	gas-vesicle protei
32	15	100.0	40	2	I41476	probable antigen 9
33	15	100.0	40	2	T07583	hypothetical prote
34	15	100.0	40	2	T07574	hypothetical prote
35	15	100.0	40	2	A82529	trypsin inhibitor
36	15	100.0	41	1	T172	trypsin inhibitor
37	15	100.0	41	2	S77772	ribose-phosphate p
38	15	100.0	42	2	I65746	tropomyosin - huma
39	15	100.0	43	2	S42852	mela protein - Sal
40	15	100.0	44	2	F81839	hypothetical prote
41	15	100.0	45	2	D82399	hypothetical prote
42	15	100.0	46	2	PC4400	crotoxin-binding p
43	15	100.0	47	2	S78708	protein YBR126w-a
44	15	100.0	48	2	S19612	chlorophyll a/b-bi
45	15	100.0	50	2	H90760	hypothetical prote

ALIGNMENTS

RESULT 1  
A60624  
angiotensin I - Japanese quail  
C:Species: Coturnix coturnix japonica (Japanese quail)  
C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-May-1999  
C:Accession: A60624  
R:Takai, Y.; Hasegawa, Y.  
Gen. Comp. Endocrinol. 79, 12-22, 1990  
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of t  
A:Reference number: A60624; MUID:90284684  
A:Accession: A60624  
A:Molecule type: protein  
A:Residues: 1-10 <RAK>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 100.0%; Score 15; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 2  
S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432  
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen  
Eur. J. Biochem. 237, 414-423, 1996  
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipt  
A:Reference number: S65431; MUID:96215437  
A:Accession: S65432  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <WJ>  
A:Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 15; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 3  
A90917  
angiotensin precursor - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A90917; A01250  
R:Nakayama, T.; Nakajima, T.; Sokabe, H.  
Chem. Pharm. Bull. 21, 2085-2087, 1973  
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its  
A:Reference number: A90917; MUID:74127845  
A:Accession: A90917  
A:Molecule type: protein  
A:Residues: 1-10 <NAK>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 15; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 4  
A90345  
angiotensin precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A90345; A01250  
R:Elliot, D.F.; Peart, W.S.  
Biochem. J. 65, 246-254, 1957  
A:Title: The amino acid sequence in a hypertensin.  
A:Reference number: A90345  
A:Accession: A90345  
A:Molecule type: protein  
A:Residues: 1-10 <ELL>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 15; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 5  
A01250  
angiotensin precursor - horse (fragment)  
C:Species: Equus caballus (domestic horse)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998  
C:Accession: A92775; A01250  
R:Skeggis Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957  
A:Reference number: A92775  
A:Accession: A92775  
A:Molecule type: protein  
A:Residues: 1-14 <SKE>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 15; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DRV 3  
|||  
Db 1 DRV 3  
RESULT 6  
A60834  
angiotensin I precursor - dog (fragment)  
N:Alternate names: angiotensinogen I  
N:Contains: angiotensin I  
C:Species: Canis lupus familiaris (dog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1998  
C:Accession: A60834  
R:Oliver, J.A.  
Hypertension 11, 21-27, 1988  
A:Title: Purification and partial characterization of canine angiotensinogen.  
A:Reference number: A60834; MUID:88113996  
A:Accession: A60834  
A:Molecule type: protein  
A:Residues: 1-15 <OLI>  
C:Superfamily: antithrombin III  
C:Keywords: glycoprotein; plasma  
F:1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 7  
PA0041  
plastoquinol--plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C:Accession: PA0041  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi  
A:Reference number: PA0001  
A:Accession: PA0041  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>  
A:Experimental source: leaf  
C:Keywords: oxidoreductase

Query Match 100.0%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 7 DRV 9

RESULT 8  
H75063  
hypothetical protein PAH7382 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
C:Accession: H75063  
R:anonymous; Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s  
A:Reference number: A75001

A:Accession: H75063  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-18 <KAW>  
A:Cross-references: GB:AJ248287; GB:AL096836; NID:95458657; PIDN:CAB50405.1; PID:el51630  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB7382

Query Match 100.0%; Score 15; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 11 DRV 13

RESULT 9  
A31049  
calsequestrin, fast skeletal muscle - rat (fragment)  
N:Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 16-Jul-1999  
C:Accession: A31049; S46193; S46194; S46195  
R:Hall, D.E.; Frazer, K.A.; Hann, B.C.; Reichardt, L.F.  
J. Cell Biol. 107, 687-697, 1988

A:Title: Isolation and characterization of a laminin-binding protein from rat and chick  
A:Reference number: A92751; MUID:88331073

A:Accession: A31049  
A:Molecule type: protein  
A:Residues: 1-20 <HAL>  
R:Volpe, P.; Martini, A.; Furlan, S.; Meldolesi, J.  
Biochem. J. 301, 465-469, 1994

A:Title: Calsequestrin is a component of smooth muscles: the skeletal- and cardiac-muscle  
A:Reference number: S46193; MUID:94318050

A:Accession: S46193  
A:Molecule type: protein  
A:Residues: 1-9 <VOL>  
A:Accession: S46194  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 'XX',4-10,'X',12 <VO2>  
A:Accession: S46195  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 'XE',3-12 <VO3>

C:Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protein  
C:Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to c  
C:Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi  
C:Superfamily: calsequestrin  
C:Keywords: calcium binding; glycoprotein; skeletal muscle

Query Match 100.0%; Score 15; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 13 DRV 15

RESULT 10  
A05313  
apolipoprotein A-I - red guenon (fragment)  
N:Alternate names: apo-A-I  
C:Species: Erythrocebus patas (red guenon, hussar)  
C>Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 11-May-2000  
C:Accession: A05313  
R:Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.  
Biochemistry 15, 1928-1933, 1976

A:Title: Characterization of the plasma lipoproteins and apoproteins of the Erythroce  
A:Reference number: A90395; MUID:76184721  
A:Accession: A05313  
A:Molecule type: protein  
A:Residues: 1-20 <MAH>  
C:Superfamily: apolipoprotein A-I  
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; 1

Query Match 100.0%; Score 15; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 9 DRV 11

RESULT 11  
S03987  
agglutinin beta-2 chain - Osage orange  
C:Species: Maclura pomifera (Osage orange)  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
C:Accession: S03987  
R:Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.  
Arch. Biochem. Biophys. 270, 596-603, 1989  
A:Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia an  
A:Reference number: S03983; MUID:89206218

A:Accession: S03987  
A:Molecule type: protein  
A:Residues: 1-20 <YOU>

Query Match 100.0%; Score 15; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 16 DRV 18

RESULT 12  
S03986  
agglutinin beta-1 chain - Osage orange  
C:Species: Maclura pomifera (Osage orange)  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 01-Aug-1997  
C:Accession: S03986; S03988  
R:Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.  
Arch. Biochem. Biophys. 270, 596-603, 1989  
A:Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia an  
A:Reference number: S03983; MUID:89206218

A:Accession: S03986  
A:Molecule type: protein  
A:Residues: 1-21 <YOU>  
A:Note: beta-1 form  
A:Accession: S03988  
A:Molecule type: protein  
A:Residues: 2-21 <YO2>  
A:Note: beta-3 form

Query Match 100.0%; Score 15; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 17 DRV 19

RESULT 13  
B39313

chaperonin, 10K - Thermus aquaticus (fragment)  
C:Species: Thermus aquaticus  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 16-Feb-1997  
C:Accession: B39313  
R:Taguchi, H.; Konishi, J.; Ishii, N.; Yoshida, M.  
J. Biol. Chem. 266, 22411-22418, 1991  
A:Title: A chaperonin from a thermophilic bacterium, Thermus thermophilus, that controls  
A:Reference number: A39313; MUID:92042183  
A:Accession: B39313  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-23 <TAG>  
C:Keywords: molecular chaperone

Query Match 100.0%; Score 15; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 13 DRV 15

## RESULT 14

C49732  
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 29K chain - potato mitochondrion (fragment)  
N:Alternate names: complex 1 dehydrogenase 29K chain; NADH-ubiquinone oxidoreductase 29K  
C:Species: mitochondrion Solanum tuberosum (potato)  
C:Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 07-May-1999  
C:Accession: C49732  
R:Herz, U.; Schroeder, W.; Liddell, A.; Leaver, C.J.; Brennicke, A.; Grohmann, L.  
J. Biol. Chem. 269, 2263-2269, 1994  
A:Title: Purification of the NADH:ubiquinone oxidoreductase (complex I) of the respiratory  
A:Reference number: A49732; MUID:94124587  
A:Accession: C49732  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-23 <HER>  
C:Genetics:  
A:Genome: mitochondrion  
C:Keywords: electron transfer; hydrogen ion transport; mitochondrial inner membrane; mit

Query Match 100.0%; Score 15; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 13 DRV 15

## RESULT 15

A60502  
myonexin - northern leopard frog (fragment)  
C:Species: Rana pipiens (northern leopard frog)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Jul-1999  
C:Accession: A60502; A33087  
R:Tidball, J.G.  
Dev. Biol. 142, 103-114, 1990  
A:Title: Myonexin: an 80-kDa glycoprotein that binds fibronectin and is located at embry  
A:Reference number: A60502; MUID:91032554  
A:Accession: A60502  
A:Molecule type: protein  
A:Residues: 1-25 <TID>  
C:Comment: This protein resembles calsequestrin in sequence but differs in distribution  
C:Superfamily: calsequestrin  
C:Keywords: fibronectin binding; glycoprotein; skeletal muscle

Query Match 100.0%; Score 15; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRV 3  
|||  
Db 13 DRV 15

Search completed: July 1, 2002, 07:46:32  
Job time: 453 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:10 ; Search time 34.05 seconds  
(without alignments)  
3.411 Million cell updates/sec

Title: US-09-723-197-11

Perfect score: 15  
Sequence: 1 DRV 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
2	15	100.0	10	1 ANG1_BOTJA	Q10581 bothrops ja
3	15	100.0	10	1 ANG1_BOVIN	P01017 bos taurus
4	15	100.0	10	1 ANG1_CHICK	P01018 gallus gall
5	15	100.0	14	1 ANG1_HORSE	P01016 equus caball
6	15	100.0	19	1 FUBB_LAMGL	P14473 lama glama
7	15	100.0	20	1 APAL_ERIPA	P18647 erythrocebu
8	15	100.0	20	1 CAQS_RAT	P19633 rattus norv
9	15	100.0	20	1 LEC2_MACPO	P18676 maciura pom
10	15	100.0	20	1 LEC3_MACPO	P18677 maciura pom
11	15	100.0	20	1 PGK_BACCE	P83075 bacillus ce
12	15	100.0	21	1 CH1C_PEA	P31233 pisum sativ
13	15	100.0	21	1 LEC1_MACPO	P18675 maciura pom
14	15	100.0	23	1 NUO5_SOLTU	P80262 solanum tub
15	15	100.0	26	1 AMD1_CHICK	P81073 gallus gall
16	15	100.0	26	1 AMD1_RABIT	P81072 oryctolagus
17	15	100.0	38	1 PSBX_ODOSI	P49509 odontella s
18	15	100.0	39	1 PSBX_GULTH	O78455 quillardia
19	15	100.0	41	1 ITRY_TRIKI	P01069 trichosanth
20	15	100.0	43	1 VPU_HVIC4	P08803 human immun
21	15	100.0	49	1 R331_BACSU	P56849 bacillus su
22	15	100.0	54	1 VPW_BIV27	P24034 bovine immu
23	15	100.0	55	1 RMF_ECOLI	P22986 escherichia
24	15	100.0	56	1 CAQS_CANFA	P31236 canis famil
25	15	100.0	57	1 Y160_ARCFU	O28419 archaeoglob
26	15	100.0	58	1 ACEA_HELAN	P20699 helianthus
27	15	100.0	61	1 PPSA_ERWHE	O54457 erwinia her
28	15	100.0	62	1 DSRB_ECOLI	P40678 escherichia
29	15	100.0	63	1 YOR4_TTV1	P19279 thermoprote
30	15	100.0	64	1 SCX5_ANDMA	P01482 androctonus
31	15	100.0	64	1 SCX5_LEIOU	P01481 leirurus qui
32	15	100.0	65	1 RL35_BUCAI	P57227 buchnera ap
33	15	100.0	65	1 SCX3_MESMA	P15227 mesobuthus

34	15	100.0	66	1 Y13G_BPT4	P39500 bacterioph
35	15	100.0	67	1 CSPA_MICLU	Q10875 micrococcus
36	15	100.0	67	1 SCX3_ORTSC	P15225 orthochirus
37	15	100.0	67	1 YPUB_BACSU	P35151 bacillus su
38	15	100.0	68	1 BGIA_MOMCH	P24076 momordica c
39	15	100.0	69	1 ACP_RHOSH	P12784 rhodobacter
40	15	100.0	69	1 ATSI_AMACA	P80211 amaranthus
41	15	100.0	69	1 ICI_LINUS	P82381 linum usita
42	15	100.0	70	1 FLC1_ECOLI	P11519 escherichia
43	15	100.0	70	1 FLC2_ECOLI	P23587 escherichia
44	15	100.0	70	1 Y4ON_RHISN	P55599 rhizobium s
45	15	100.0	71	1 CHH1_MACRS	P81206 macrobrachi

ALIGNMENTS

RESULT 1  
ANG2\_BOTJA  
ID ANG2\_BOTJA STANDARD; PRT; 8 AA.  
AC Q10582;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide II (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
RT "Isolation and identification of angiotensin-like peptides from the  
plasma of the snake Bothrops jararaca.";  
RL Comp. Biochem. Physiol. 113B:467-473(1996).  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 15; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. le+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRV 3  
Db 1 DRV 3

RESULT 2  
ANG1\_BOTJA  
ID ANG1\_BOTJA STANDARD; PRT; 10 AA.  
AC Q10581;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide I (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

RT "Isolation and identification of angiotensin-like peptides from the  
 RL plasma of the snake Bothrops jararaca."  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 DB 1 DRV 3

## RESULT 3

ANGT\_BOVIN STANDARD; PRT; 10 AA.  
 AC P01017;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN8 OR AGT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RA Elliott D.F., Peart W.S.;  
 RT "The amino acid sequence in a hypertensin."  
 RL Biochem. J. 65:246-254(1957).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A01250; A01250.  
 DR PIR; A0345; A0345.

DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1282 MW; CEF5DD761F2DB42 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 DB 1 DRV 3

## RESULT 4

ANGT\_CHICK STANDARD; PRT; 10 AA.  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN8 OR AGT.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 93934;  
 RN [1]  
 RP SEQUENCE.

RC SPECIES=Chicken;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sokabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of fowl  
 RT angiotensin and its identification by DNS-method."  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RN [2]  
 RP SEQUENCE.

RC SPECIES=C.c.japonica;  
 RX MEDLINE=90284684; PubMed=2191893;  
 RA Takei Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and  
 RT inhibition of these effects in the Japanese quail."  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A01250; A01250.  
 DR PIR; A0917; A0917.  
 DR PIR; A60624; A60624.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.

KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; CEF5DD761F2DB42 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 DB 1 DRV 3

## RESULT 5

ANGT\_HORSE STANDARD; PRT; 14 AA.  
 AC P01016;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN8 OR AGT.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE.

RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;  
 RT "The preparation, purification, and amino acid sequence of a  
 RT polypeptide renin substrate."  
 RL J. Exp. Med. 106:439-453(1957).



CC -|- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -|- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR: A01250; A01250. Serpin.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBD7 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
Db 1 DRV 3

## RESULT 6

ID FIBB\_LAMGL STANDARD; PRT; 19 AA.  
AC P14473;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Lama glama (Llama),  
OS Lama vicugna (Vicugna vicugna), and  
OS Camelus dromedarius (Dromedary) (Arabian camel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.  
OX NCBI\_TaxID=9844, 9843, 9838;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=L.glama;  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals."  
RL Acta Chem. Scand. 19:1789-1791(1965).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C. dromedarius;  
RX MEDLINE=67209145; PubMed=6033721;  
RA Doolittle R.F., Schubert D., Schwartz S.A.;  
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.  
RT Dromedary camel, mule deer, and cape buffalo."  
RL Arch. Biochem. Biophys. 118:456-467(1967).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.vicugna;  
RA Moss G.A., Doolittle R.F.;  
RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";  
RL Arch. Biochem. Biophys. 122:674-684(1967).

CC -|- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.

CC -|- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -|- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR InterPro: IPR002181; Fibrinogen\_C.  
DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.

KW Blood coagulation; Plasma; Sulfation.  
FT PEPTIDE 1 19 FIBRINOPEPTIDE B.  
FT MOD\_RES 4 4 SULFATION.  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2295 MW; E7E6B6100568638 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
Db 10 DRV 12

## RESULT 7

ID APA1\_ERYPA STANDARD; PRT; 20 AA.  
AC P18647;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Apolipoprotein A-I (Apo-AI) (Fragment).  
GN APOA1.  
OS Erythrocebus patas (Red guenon) (Hussar).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Erythrocebus.  
OX NCBI\_TaxID=9538;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76184721; PubMed=178359;  
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;  
RT "Characterization of the plasma lipoproteins and apoproteins of the  
RT Erythrocebus patas monkey."  
RL Biochemistry 15:1928-1933(1976).  
CC -|- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF  
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING  
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR  
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).  
CC -|- SUBCELLULAR LOCATION: Extracellular.  
CC -|- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN  
CC CHYLOMICRONS.  
CC -|- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.  
DR PIR: A05313; A05313.  
KW Plasma; Lipid transport; HDL; Cholesterol metabolism.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 100.0%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
Db 9 DRV 11

## RESULT 8

ID CAQS\_RAT STANDARD; PRT; 20 AA.  
AC P19633;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Caldesmon, skeletal muscle isoform (Aspartactin) (Laminin-binding  
DE protein) (Fragment).  
GN CASQ1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88331073; PubMed=3417768;  
RA Hall D.E., Frazer K.A., Hann B.C., Reichardt L.F.;  
RT "Isolation and characterization of a laminin-binding protein from rat  
J. Cell Biol. 107:687-697(1988)."  
RL  
CC -1- FUNCTION: CALSEQUESTRIN IS A HIGH-CAPACITY, MODERATE AFFINITY,  
CC CALCIUM-BINDING PROTEIN AND THUS ACTS AS AN INTERNAL CALCIUM STORE  
CC IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSEQUESTRIN THROUGH  
CC A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40  
CC TO 50 MOLES OF CALCIUM. ALSO BINDS LAMININ.  
CC -1- SUBCELLULAR LOCATION: THIS ISOFORM OF CALSEQUESTRIN OCCURS IN THE  
CC SARCOPLASMIC RETICULUM'S TERMINAL CISTERNAE LUMINAL SPACES OF  
CC FAST SKELETAL MUSCLE CELLS. ASPARTACTIN IS FOUND IN THE BASAL  
CC LAMINA SURROUNDING INDIVIDUAL MUSCLE FIBERS.  
CC -1- TISSUE SPECIFICITY: SKELETAL AND HEART MUSCLE.  
CC -1- SIMILARITY: BELONGS TO THE CALSEQUESTRIN FAMILY.  
DR PIR; A31049; A31049.  
DR HSP; P07221; 1A8Y.  
DR InterPro: IPR001393; Calsequestrin.  
DR PROSITE; PS00864; CALSEQUESTRIN\_2; PARTIAL.  
DR PROSITE; PS00863; CALSEQUESTRIN\_1; 1.  
KW Muscle; Glycoprotein; Calcium-binding.  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2238 MW; 92ADE04FC2A69280 CRC64;  
  
Query Match 100.0%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRV 3  
Db 13 DRV 15  
[1]  
  
RESULT 9  
LEC2\_MACPO STANDARD; PRT; 20 AA.  
AC P18676;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DE Agglutinin beta-2 chain (MPA).  
OS Maclura pomifera (Osage orange).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Moraceae; Maclura.  
OX NCBI\_TaxID=3496;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Seed;  
RX MEDLINE=89206218; PubMed=2705782;  
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;  
RT "Homology of the D-galactose-specific lectins from Artocarpus  
integrifolia and Maclura pomifera and the role of an unusual small  
polypeptide subunit.";  
RL Arch. Biochem. Biophys. 270:596-603(1989).  
CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN  
CC SUBUNIT. FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.  
CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
DR PIR; S03988; S03988.  
DR HSP; P18676; 1JOT.  
KW Lectin.  
SQ SEQUENCE 20 AA; 2082 MW; AA38811BBD6370E0 CRC64;  
  
Query Match 100.0%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRV 3  
Db 16 DRV 18  
[1]  
  
RESULT 11  
PGK\_BACCE STANDARD; PRT; 20 AA.  
ID P83075;  
AC P83075;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phosphoglycerate kinase (EC 2.7.2.3) (Fragment).  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE, AND INDUCTION.  
RC STRAIN=NCIMB 11796;  
RA Browne N., Dowds B.C.A.;  
RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-

DR PDB; 1JOT; 16-FEB-99.  
KW Lectin; 3D-structure.  
SQ SEQUENCE 20 AA; 2141 MW; AA3882AD5D6370E0 CRC64;  
  
Query Match 100.0%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRV 3  
Db 16 DRV 18  
[1]  
  
RESULT 10  
LEC3\_MACPO STANDARD; PRT; 20 AA.  
ID P18677;  
AC P18677;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DE Agglutinin beta-3 chain (MPA).  
OS Maclura pomifera (Osage orange).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Moraceae; Maclura.  
OX NCBI\_TaxID=3496;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Seed;  
RX MEDLINE=89206218; PubMed=2705782;  
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;  
RT "Homology of the D-galactose-specific lectins from Artocarpus  
integrifolia and Maclura pomifera and the role of an unusual small  
polypeptide subunit.";  
RL Arch. Biochem. Biophys. 270:596-603(1989).  
CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN  
CC SUBUNIT. FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.  
CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
DR PIR; S03988; S03988.  
DR HSP; P18676; 1JOT.  
KW Lectin.  
SQ SEQUENCE 20 AA; 2082 MW; AA38811BBD6370E0 CRC64;  
  
Query Match 100.0%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DRV 3  
Db 16 DRV 18  
[1]  
  
RESULT 11  
PGK\_BACCE STANDARD; PRT; 20 AA.  
ID P83075;  
AC P83075;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phosphoglycerate kinase (EC 2.7.2.3) (Fragment).  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE, AND INDUCTION.  
RC STRAIN=NCIMB 11796;  
RA Browne N., Dowds B.C.A.;  
RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-

CC phospho-D-glyceroyl phosphate.  
 CC -!- PATHWAY: Second step in the second phase of glycolysis.  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- INDUCTION: By heat shock.  
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.  
 DR InterPro: IPR001576; PKG.  
 DR PROSITE: PS00111; POLYMERASE\_KINASE; PARTIAL.  
 KW Transferase; Kinase; Glycolysis; Heat shock.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2403 MW; EDAD2CAF1155C353 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
 Db 18 DRV 20

RESULT 12  
 CHIC\_PEA  
 ID CHIC\_PEA STANDARD; PRT; 21 AA.  
 AC P31233;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 20 kDa chaperonin, chloroplast (protein Cpn21) (Chloroplast protein Cpn10) (Chloroplast chaperonin 10) (Ch-Cpn10) (Fragment).  
 DE Cpn21 OR CHCPN10.  
 GN Pisum sativum (Garden pea).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92409583; PubMed=1356267;  
 RA Bertsch U., Soll J., Seetharam R., Viitanen P.V.;  
 RT Identification, characterization, and DNA sequence of a functional 'double' groes-like chaperonin from chloroplasts of higher plants.;  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8696-8700(1992).  
 CC -!- FUNCTION: SEEMS TO FUNCTION ONLY AS A COCHAPERONIN, ALONG WITH CPN60, AND IN CERTAIN CASES IS ESSENTIAL FOR THE DISCHARGE OF BIOLOGICALLY ACTIVE PROTEINS FROM CPN60.  
 CC -!- SUBUNIT: FORMS STABLE COMPLEXES WITH CPN60 IN THE PRESENCE OF ATP.  
 CC -!- SUBCELLULAR LOCATION: Chloroplast.  
 CC -!- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.  
 DR InterPro: IPR001476; Cpn10.  
 DR Pfam: PF00166; cpn10; 1.  
 DR PROSITE: PS00681; CHAPERONINS\_CPN10; PARTIAL.  
 DR Chaperone; Chloroplast.  
 FT NON\_TER 21  
 SQ SEQUENCE 21 AA; 2240 MW; 260295B3C087FD95 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
 Db 16 DRV 18

RESULT 13  
 LEC1\_MACPO  
 ID LEC1\_MACPO STANDARD; PRT; 21 AA.  
 AC P18675;  
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Agglutinin beta-1 chain (MPA).  
 OS Maclura pomifera (Osage orange).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Moraceae; Maclura.  
 OX NCBI\_TaxID=3496;  
 RN [1]  
 RP SEQUENCE.  
 RT TISSUE=Seed;  
 RX MEDLINE=89206218; PubMed=2705782;  
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;  
 RT Homology of the D-galactose-specific lectins from Artocarpus integrifolia and Maclura pomifera and the role of an unusual small polypeptide subunit.;  
 RL Arch. Biochem. Biophys. 270:596-603(1989).  
 CC -!- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN STRUCTURE GAL-BETA1-3-GALNAC.  
 CC -!- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.  
 CC -!- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
 DR PIR: S03986; S03986.  
 DR HSP; P18676; LUOT.  
 KW Lectin.  
 SQ SEQUENCE 21 AA; 2196 MW; AA38811BC1BFD0E0 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
 Db 17 DRV 19

RESULT 14  
 NU05\_SOLTU  
 ID NU05\_SOLTU STANDARD; PRT; 23 AA.  
 AC P80262;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 29 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-29KD) (CI-29KD) (Fragment).  
 DE Solanum tuberosum (Potato).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=CV. BINTJE; TISSUE=Tuber;  
 RX MEDLINE=94124587; PubMed=6294484;  
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A., Grobmann L.;  
 RT Purification of the NADH:ubiquinone oxidoreductase (complex I) of the respiratory chain from the inner mitochondrial membrane of Solanum tuberosum.;  
 RL J. Biol. Chem. 269:2263-2269(1994).  
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER MEMBRANE.  
 DR PIR: C49732; C49732.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
 FT NON\_TER 23  
 SQ SEQUENCE 23 AA; 2653 MW; 4B41B8FF83412F58 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 Db 13 DRV 15

RESULT 15  
 AMD1\_CHICK  
 ID AMD1\_CHICK STANDARD; PRT; 26 AA.  
 AC P81073;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE AMP deaminase 1 (EC 3.5.4.6) (Myoadenylate deaminase) (AMP deaminase  
 isoform M) (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Breast;  
 RX MEDLINE=97269365; PubMed=9114497;  
 RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;  
 RT "AMP-deaminases from chicken and rabbit muscle: partial primary  
 sequences of homologous 17-kDa CNBr fragments: autorecognition by  
 rabbit anti-[chicken AMP]";  
 RL Comp. Biochem. Physiol. 116B:371-377(1997).  
 CC -!- FUNCTION: AMP DEAMINASE PLAYS A CRITICAL ROLE IN ENERGY  
 METABOLISM  
 CC -!- CATALYTIC ACTIVITY: AMP + H(2)O = IMP + NH(3).  
 CC -!- PATHWAY: PURINE NUCLEOTIDE CYCLE.  
 CC -!- SUBUNIT: HOMOTETRAMER.  
 CC -!- SIMILARITY: BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.  
 DR InterPro: IPR001365; A\_deaminase.  
 DR PROSITE: PS00485; A\_DEAMINASE; PARTIAL.  
 KW Hydrolase; Nucleotide metabolism; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 26  
 SQ SEQUENCE 26 AA; 3195 MW; B03E296D63BB6E75 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 Db 19 DRV 21

Search completed: July 1, 2002, 07:47:11  
 Job time: 477 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:16 ; Search time 122.73 Seconds

(without alignments)  
4.229 Million cell updates/sec

Title: us-09-723-197-11

Perfect score: 15

Sequence: 1 DRV 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	15	100.0	9	12 Q83622	Q83622 murray vall
2	15	100.0	10	13 Q9PS07	Q9PS07 alligator m
3	15	100.0	14	5 Q10757	Q10757 theromyzon
4	15	100.0	15	2 Q9R4K0	Q9R4K0 nocardia. n
5	15	100.0	15	2 Q9R521	Q9R521 francisella
6	15	100.0	15	2 Q05931	Q05931 staphylococ
7	15	100.0	16	1 Q9UWJ4	Q9UWJ4 pyrococcus
8	15	100.0	17	12 Q89807	Q89807 epiphyas po
9	15	100.0	18	4 Q9BU72	Q9BU72 homo sapien
10	15	100.0	18	17 Q9UYK7	Q9UYK7 pyrococcus
11	15	100.0	19	10 P83089	P83089 spinacia ol
12	15	100.0	19	11 Q9Z115	Q9Z115 rattus sp.
13	15	100.0	20	2 Q9R519	Q9R519 mycobacteri
14	15	100.0	20	11 Q9QVGO	Q9QVGO rattus sp.
15	15	100.0	22	2 Q47529	Q47529 escherichia
16	15	100.0	24	8 Q9T2H3	Q9T2H3 spinacia ol

17	15	100.0	25	2 Q51310	Q51310 nostoc sp.
18	15	100.0	26	4 Q9UCT8	Q9UCT8 homo sapien
19	15	100.0	27	12 Q56510	Q56510 hepatitis c
20	15	100.0	28	4 Q96F68	Q96F68 homo sapien
21	15	100.0	29	4 Q9UEF0	Q9UEF0 homo sapien
22	15	100.0	29	5 Q9TX02	Q9TX02 chironomus
23	15	100.0	29	12 Q919A6	Q919A6 porcine rep
24	15	100.0	31	11 Q99PC8	Q99PC8 rattus norv
25	15	100.0	33	8 Q9T2N1	Q9T2N1 nicotiana t
26	15	100.0	33	8 Q9T2M1	Q9T2M1 nicotiana t
27	15	100.0	33	11 Q62676	Q62676 rattus norv
28	15	100.0	35	10 Q9FJ84	Q9FJ84 arabidopsis
29	15	100.0	35	10 Q9LV08	Q9LV08 arabidopsis
30	15	100.0	35	10 Q92UM2	Q92UM2 arabidopsis
31	15	100.0	35	13 Q90XB5	Q90XB5 xenopus lae
32	15	100.0	35	16 Q9KQK2	Q9KQK2 vibrio chol
33	15	100.0	36	2 Q68947	Q68947 azomonas ma
34	15	100.0	36	10 Q42333	Q42333 arabidopsis
35	15	100.0	36	16 Q9PGM9	Q9PGM9 xylella fas
36	15	100.0	36	16 Q9KQ35	Q9KQ35 vibrio chol
37	15	100.0	38	12 Q9WNW6	Q9WNW6 japanese en
38	15	100.0	38	16 Q9PFK7	Q9PFK7 xylella fas
39	15	100.0	38	16 Q99U43	Q99U43 staphylococ
40	15	100.0	39	2 Q9RIJ8	Q9RIJ8 streptococc
41	15	100.0	39	16 Q31492	Q31492 bacillus su
42	15	100.0	40	2 Q9KZ25	Q9KZ25 streptomyce
43	15	100.0	40	7 Q62886	Q62886 canis famil
44	15	100.0	40	8 Q32999	Q32999 pinus thunb
45	15	100.0	40	8 Q33006	Q33006 pinus thunb

ALIGNMENTS

RESULT 1

Q83622	PRELIMINARY;	PRT;	9 AA.
AC Q83622			
DT 01-NOV-1996 (Tremblrel. 01, Created)			
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE HYPOTHETICAL 1.1 KDA PROTEIN (FRAGMENT).			
OS Murray valley encephalitis virus.			
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;			
OC Flavivirus.			
OX NCBI_TaxID=11079;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=88118912; PubMed=2828633;			
RA Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L., Strauss E.G.,			
RA Strauss J.H.;			
RT "Conserved elements in the 3' untranslated region of flavivirus RNAs			
RT and potential cyclization sequences.";			
RL J. Mol. Biol. 198:33-41(1987).			
DR EMBL; M35172; AAA66627.1; -			
KW Hypothetical protein.			
FT NON_TER 1			
SQ SEQUENCE 9 AA; 1055 MW; FF36D40AAB05A2C1 CRC64;			

Query Match 100.0%; Score 15; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
Db 6 DRV 8

RESULT 2

Q9PS07	PRELIMINARY;	PRT;	10 AA.
ID Q9PS07			
AC Q9PS07;			

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE ANGIOTENSIN I, ANG I.  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylia; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93307610; PubMed=8319878;  
RA Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,  
RA Stephens G.A., Sakakibara S.;  
RT "New angiotensin I isolated from a reptile, Alligator  
RT mississippiensis."  
RL Gen. Comp. Endocrinol. 90:214-219(1993).  
SQ SEQUENCE 10 AA; 1216 MW; CE38DD761F2DB42 CRC64;

Query Match 100.0%; Score 15; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 3  
Q10757  
ID Q10757 PRELIMINARY; PRT; 14 AA.  
AC Q10757;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE ANGIOTENSINOGEN (FRAGMENT).  
OS Theromyzon tessulatum (Leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
OX NCBI\_TaxID=13286;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95365039; PubMed=7637887;  
RA Laurent V., Bulet P., Salzert M.A.;  
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like  
RT molecule with forms of vertebrate angiotensinogens: a hormonal system  
RT conserved in the course of evolution."  
RL Neurosci. Lett. 190:175-178(1995).  
RN [2]  
RP SEQUENCE OF 1-10.  
RC TISSUE=BRAIN;  
RX MEDLINE=96201949; PubMed=8612806;  
RA Laurent V., Salzert M.;  
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon  
RT tessulatum."  
RL FEBS Lett. 384:123-127(1996).  
CC -I- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.  
KW Glycoprotein; Serpin.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEFBD7 CRC64;

Query Match 100.0%; Score 15; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 1 DRV 3

RESULT 4  
Q94K0  
ID Q94K0 PRELIMINARY; PRT; 15 AA.

ID Q94K0 PRELIMINARY; PRT; 15 AA.  
AC Q94K0;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE NITRIC OXIDE SYNTHASE (EC 4.14.23.-).  
OS Nocardia.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Nocardiaceae.  
OX NCBI\_TaxID=1817;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95394819; PubMed=7545152;  
RA Chen Y., Rosazza J.P.;  
RT "Purification and characterization of nitric oxide synthase (NOSNoc)  
RT from a Nocardia species."  
RL J. Bacteriol. 177:5122-5128(1995).  
SQ SEQUENCE 15 AA; 1818 MW; 2BD58859DE288B77 CRC64;

Query Match 100.0%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 10 DRV 12

RESULT 5  
Q9R521  
ID Q9R521 PRELIMINARY; PRT; 15 AA.  
AC Q9R521;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE GROES HOMOLOG (FRAGMENT).  
OS Francisella tularensis.  
OC Bacteria; Proteobacteria; gamma subdivision; Francisella group;  
OC Francisella.  
OX NCBI\_TaxID=263;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94086099; PubMed=7903283;  
RA Ericsson M., Tarnvik A., Kuoppa K., Sandstrom G., Sjostedt A.;  
RT "Increased synthesis of DnaK, GroEL, and GroES homologs by Francisella  
RT tularensis LVS in response to heat and hydrogen peroxide."  
RL Infect. Immun. 62:178-183(1994).  
DR InterPro: IPR001476; Cpn10.  
DR Pfam: PF00166; Cpn10; 1.  
SQ SEQUENCE 15 AA; 1837 MW; 9DCF2D4507437D33 CRC64;

Query Match 100.0%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
|||  
Db 8 DRV 10

RESULT 6  
O05991  
ID O05991 PRELIMINARY; PRT; 15 AA.  
AC O05991;  
DT 01-JUL-1997 (TReMBLrel. 04, Created)  
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE SIMILAR TO BIN3 AND SIN RECOMBINASES OF STAPHYLOCOCCUS AUREUS  
DE (FRAGMENT).  
OS Staphylococcus simulans.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1286;  
RN [1]  
RP SEQUENCE FROM N.A. PubMed-9106216;  
RX MEDLINE=97260121; PubMed-9106216;  
RA Thumm G., Gotz F.;

RT "Studies on prollystaphin processing and characterization of the  
RT lysostaphin immunity factor (Lif) of Staphylococcus simulans biovar  
RT staphylolyticus";  
RL Mol. Microbiol. 23:1251-1265(1997).  
DR EMBL; U66883; AAB53786.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1808 MW; 1D1A4AB1EE1E3CFF CRC64;

Query Match 100.0%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
Db 13 DRV 15

RESULT 7

Q9UWJ4 PRELIMINARY; PRT; 16 AA.  
AC Q9UWJ4;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE SULFIDE DEHYDROGENASE ALPHA SUBUNIT (FRAGMENT).  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95050208; PubMed=7961401;  
RA Ma K., Adams M.W.;  
RT "Sulfide dehydrogenase from the hyperthermophilic archaeon Pyrococcus  
RT furiosus: a new multifunctional enzyme involved in the reduction of  
RT elemental sulfur.";  
RL J. Bacteriol. 176:6509-6517(1994).  
SQ SEQUENCE 16 AA; 1909 MW; 47EAAB14F8F6744A CRC64;

Query Match 100.0%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
Db 5 DRV 7

RESULT 8

O89807 PRELIMINARY; PRT; 17 AA.  
AC O89807;  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE LATE EXPRESSION FACTOR-1 (FRAGMENT).  
GN LEF-1.  
OS Epiphyas postvittana nucleopolyhedrovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
OC Nucleopolyhedrovirus.  
OX NCBI\_TaxID=70600;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21342908; PubMed=11450943;  
RA Caradoc-Davies K.M., Graves S., O'Reilly D.R., Evans O.P., Ward V.K.;

RT "Identification and in vivo characterization of the Epiphyas

RT postvittana nucleopolyhedrovirus Ecdysteroid UDP-  
RT glucosyltransferase";  
RL Virus Genes 22:255-264(2001).  
DR EMBL; AF052502; AAC34492.1; -.  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 2109 MW; 027F53CB5536F80 CRC64;

Query Match 100.0%; Score 15; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
Db 9 DRV 11

RESULT 9

Q9BU72 PRELIMINARY; PRT; 18 AA.  
AC Q9BU72;  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 2.1 KDA PROTEIN (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-ENDOMETRIAL ADENOCARCINOMA;  
RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002861; AA02861.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2064 MW; 371B21FD1E289B18 CRC64;

Query Match 100.0%; Score 15; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
Db 8 DRV 10

RESULT 10

Q9UYK7 PRELIMINARY; PRT; 18 AA.  
AC Q9UYK7;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE HYPOTHETICAL 2.1 KDA PROTEIN.  
GN PAB7382.  
OS Pyrococcus abyssi.  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
OX NCBI\_TaxID=29292;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ORSAY;  
RA Heilig R.;

RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome  
RT structure and evolution.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ248287; CAB50405.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 18 AA; 2105 MW; B53063599611DCE CRC64;

Query Match 100.0%; Score 15; DB 17; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 11 DRV 13

RESULT 11  
P83089 ID P83089 PRELIMINARY; PRT; 19 AA.  
AC P83089;  
DT 01-OCT-2001 (TREMBLrel. 18, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE 25.3 KDA PROTEIN (FRAGMENT).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE, AND SUBCELLULAR LOCATION.  
RA Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;  
RL Submitted (AUG-2001) to the SWISS-PROT data bank.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.  
KW Chloroplast. 19 19  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2093 MW; EC33422F8633F1F9 CRC64;

Query Match 100.0%; Score 15; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 14 DRV 16

RESULT 12  
Q92115 ID Q92115 PRELIMINARY; PRT; 19 AA.  
AC Q92115;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE CALCINEURIN A ALPHA (EC 3.1.3.16) (FRAGMENT).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=93111954; PubMed=1335233;  
RA Chang C., Takeda T., Mukai H., Shuntoh H., Kuno T., Tanaka C.;  
RT "Molecular cloning and characterization of the promoter region of the  
calcineurin A alpha gene.";  
RL Biochem. J. 288:801-805(1992).  
KW EMBL; D10480; BAA01283.1; -;  
KW Hydrolase.  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2115 MW; F905F8B134CCEC57 CRC64;

Query Match 100.0%; Score 15; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||

Db 15 DRV 17

RESULT 13  
Q9R519 ID Q9R519 PRELIMINARY; PRT; 20 AA.  
AC Q9R519;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE ISONICOTINATE DEHYDROGENASE (FRAGMENT).  
OS Mycobacterium.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae.  
OX NCBI\_TaxID=1763;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94103749; PubMed=8277257;  
RA Kretzer A., Frunzke K., Andreesen J.R.;  
RT "Catabolism of isonicotinate by Mycobacterium sp. INAL: extended  
description of the pathway and purification of the molybdoenzyme  
RT isonicotinate dehydrogenase".  
RL J. Gen. Microbiol. 139:2763-2772(1993).  
SQ SEQUENCE 20 AA; 2280 MW; 874DAA8637BB07C1 CRC64;

Query Match 100.0%; Score 15; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 6 DRV 8

RESULT 14  
Q9QVG0 ID Q9QVG0 PRELIMINARY; PRT; 20 AA.  
AC Q9QVG0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE CLEAVED PROLACTIN-1, CLPRL-1=FRAGMENT A.  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92143803; PubMed=1736889;  
RA Andries M., Tilemans D., Denef C.;  
RT "Isolation of cleaved prolactin variants that stimulate DNA synthesis  
RT in specific cell types in rat pituitary cell aggregates in culture.";  
RL Biochem. J. 281:393-400(1992).  
SQ SEQUENCE 20 AA; 2146 MW; 89CA019A7668CBBA CRC64;

Query Match 100.0%; Score 15; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3  
|||  
Db 18 DRV 20

RESULT 15  
Q47529 ID Q47529 PRELIMINARY; PRT; 22 AA.  
AC Q47529;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)



DE HEMA PROTEIN.  
 GN HEMA.  
 OS Escherichia coli.  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE=93171869; PubMed=7679718;  
 RA Post D.A., Hore-Jensen B., Switzer R.L.;  
 RT "Characterization of the hema-prs region of the Escherichia coli and  
 RT salmonella typhimurium chromosomes: identification of two open reading  
 RT frames and implications for prs expression."  
 RL J. Gen. Microbiol. 139:259-266(1993).  
 DR EMBL: M77237; AAA24432.1; -; 25802412BB5B4E51 CRC64;  
 SQ SEQUENCE 22 AA; 2340 MW; 25802412BB5B4E51 CRC64;

Query Match 100.0%; Score 15; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRV 3  
 Db 10 DRV 12

Search completed: July 1, 2002, 07:45:17  
 Job time: 413 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:36:08 ; Search time 158.26 Seconds  
(without alignments)  
4.913 Million cell updates/sec

Title: US-09-723-197-4  
Perfect score: 41  
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

al number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	7	17 AAR95665	Angiotensin II fra
2	41	100.0	7	19 AAW65600	Angiotensin II ana
3	41	100.0	7	19 AAW64731	Angiotensin II pep
4	41	100.0	7	19 AAW71113	Peptide AII(1-7) u
5	41	100.0	7	20 AAY49589	Angiotensin analog
6	41	100.0	7	20 AAY50296	Neutrophil-activat
7	41	100.0	7	20 AAV33904	Angiotensin II ana
8	41	100.0	7	20 AAV30542	Amino acid sequenc
9	41	100.0	7	20 AAY30586	Angiotensin II ana
10	41	100.0	7	20 AAY32717	Angiotensin II (AI
11	41	100.0	7	20 AAY33771	Angiotensin II (AI

12	41	100.0	7	20 AAY15348	Angiotensin II (AI
13	41	100.0	7	21 AAY15308	Angiotensin II (AI
14	41	100.0	7	21 AAB26205	Anion exchange res
15	41	100.0	7	21 AAB27404	Angiotensin II ana
16	41	100.0	7	21 AAB28102	Angiotensin II ana
17	41	100.0	7	21 AAY84565	Amino acid sequenc
18	41	100.0	7	21 AAY84127	Peptide comprising
19	41	100.0	7	21 AAY77040	Angiotensin II (AI
20	41	100.0	7	21 AAY57404	Angiotensin peptid
21	41	100.0	7	22 AAE08874	AII peptide (resid
22	41	100.0	7	22 AAE02991	Human angiotensin
23	41	100.0	7	22 AAE03154	Human angiotensin
24	41	100.0	7	22 AAB91463	Angiotensin peptid
25	41	100.0	8	6 AAP50467	Sequence of cyclop
26	41	100.0	8	11 AAR07584	Hypotensive polype
27	41	100.0	8	14 AAR37433	Promega peptide 8
28	41	100.0	8	16 AAR83013	Promega protein k1
29	41	100.0	8	16 AAR84269	Angiotensin II dec
30	41	100.0	8	17 AAW65193	Angiotensin II. S
31	41	100.0	8	17 AAR95662	Angiotensin II. S
32	41	100.0	8	18 AAW33309	Targetting conjuga
33	41	100.0	8	18 AAW32951	Targetting conjuga
34	41	100.0	8	18 AAW11201	Targetting conjuga
35	41	100.0	8	18 AAW14975	Conjugating peptid
36	41	100.0	8	18 AAW09656	Labelled peptide s
37	41	100.0	8	18 AAW19144	Isoelectric point
38	41	100.0	8	19 AAW65596	Angiotensin II. H
39	41	100.0	8	19 AAW65625	Angiotensin II ana
40	41	100.0	8	19 AAW64763	Angiotensin peptid
41	41	100.0	8	19 AAW64755	Angiotensin II pep
42	41	100.0	8	19 AAW64758	Angiotensin II pep
43	41	100.0	8	19 AAW64728	Angiotensin II oct
44	41	100.0	8	19 AAW65628	Angiotensin II ana
45	41	100.0	8	19 AAW71141	Angiotensin II ana

ALIGNMENTS

RESULT 1  
AAR95665  
ID AAR95665 standard; peptide; 7 AA.  
AC AAR95665;  
DT 09-JAN-1997 (first entry)  
DE Angiotensin II fragment AII(1-7).  
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;  
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;  
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.  
XX  
OS Synthetic.  
XX  
PN WO9614858-A1.  
XX  
PD 23-MAY-1996.  
XX  
PF 14-NOV-1995; 95WO-US14764.  
XX  
PR 06-JUN-1995; 95US-0465775.  
XX  
PR 14-NOV-1994; 94US-0337781.  
XX  
(UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX  
Dizerega GS, Rodgers K;  
XX  
WPI; 1996-259561/26.  
XX  
Accelerating wound healing by application of angiotensin II  
fragments - are effective at very low concn. and do not cause  
PT hypertension

XX Disclosure; Page 4; 46pp; English.

XX AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see

CC AAR95662) is an octapeptide present in humans and other species. AT2 is

CC one of the most potent vasoconstrictors known, causing constriction of

CC the arterioles. The formation of angiotensin is initiated by the action

CC of renin on angiotensinogen. The substance formed is a decapeptide

CC called angiotensin I which is converted by the enzyme angiotensinase (by

CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release

CC of extracellular matrices involved in wound repair. These fragments can

CC be used in a compound for accelerating wound healing. The compounds are

CC administered as matrical or micellar solutions, formulated with a

CC carrier or diluent, alternatively the compound is applied in conjunction

CC with a wound dressing. The carrier used in the composition is

CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly

CC glycols. By using fragments of this sequence (or analogues of it),

CC growth as well as healing of tissues is improved, such as in cases of

CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or

CC intraperitoneal surgical wounds. The compounds containing the AT2

CC fragments are less hypertensive than full length AT2, and are also

XX effective at much lower (nanomolar) concentrations than full length AT2.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVHP 7  
| | | | |  
DB 1 dryvhp 7

## RESULT 2

AAW65600  
ID AAW65600 standard; peptide; 7 AA.

AC AAW65600;

XX 09-NOV-1998 (first entry)

XX Angiotensin II analogue, AII(1-7).

XX angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;  
wound healing.

Synthetic.  
Homo sapiens.

XX W09826795-AI.

PN 25-JUN-1998.

XX 16-DEC-1997; 97WO-US23461.

XX 15-DEC-1997; 97US-0990664.

PR 16-DEC-1996; 96US-0028310.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega GS, Rodgers KE;

XX WPI; 1998-362518/31.

XX Promoting incorporation of skin graft onto underlying tissue -  
PT comprises pre-treating graft with angiotensin II, or analogue or  
PT peptide fragment

XX Disclosure; Page 6; 82pp; English.

XX The invention relates to the use of angiotensin II (AII), AII analogues,

CC AII fragments and AII fragment analogues for promoting incorporation of a  
CC skin graft into underlying tissue of a mammal. The peptides are effective  
CC in accelerating the growth or healing of skin grafts and in accelerating  
CC re-epithelialisation and tissue repair, even at very low concentrations.  
CC They can significantly accelerate the rate of healing at nanomolar levels  
CC in vivo. AII accelerates wound repair by increased neovascularisation,  
CC growth factor release, re-epithelialisation, extracellular matrix production  
CC and increased flow of blood and nutrients to the injured tissue. Use of  
CC the above peptides other than AII itself (an extremely potent vaso-  
CC constrictor) may avoid the side-effects of AII, such as increase in blood  
CC pressure and thirst. The present sequence represents an angiotensin  
CC II fragment.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVHP 7  
| | | | |  
DB 1 dryvhp 7

## RESULT 3

AAW64731  
ID AAW64731 standard; peptide; 7 AA.

XX AAW64731;

XX 02-NOV-1998 (first entry)

XX Angiotensin II peptide #3.

XX Proliferation; mesenchymal stem cell; lineage-specific cell;

KW haematopoietic; cell culture; transplantation; treatment; malignant;  
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.

XX Synthetic.

OS Homo sapiens.

XX W09832457-A2.

PN 30-JUL-1998.

XX 26-JAN-1998; 98WO-US01552.

XX 23-JAN-1998; 98US-0066593.

PR 28-JAN-1997; 97US-0036507.

PR 08-MAY-1997; 97US-0046859.

PR 28-OCT-1997; 97US-0063684.

PR 31-OCT-1997; 97US-0063910.

PR 18-NOV-1997; 97US-0065612.

PR 26-NOV-1997; 97US-0066593.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1998-437044/37.

XX Promoting haematopoietic and mesenchymal cell proliferation and  
PT differentiation - by contacting the cells with angiotensinogen,  
PT angiotensin I or II, or analogues or fragments of these

XX Claim 7; Page 14; 114pp; English.

XX AAW64728-W64763 are peptides used in a novel method for accelerating the  
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic  
CC lineage-specific cells or mesenchymal lineage-specific cells. The method  
CC involves contacting the cells with an active agent comprising a sequence  
CC consisting of at least three contiguous amino acids of groups R1-R8 in

the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val, Ala, Leu, norLeu, Ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoSer or azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Sr), Ile or Tyr, Ra and Rb are not defined in the specification, the peptide bond between Ra and Rb is labile to aminopeptidase A cleavage excluding sequences including R4 as a terminal Tyr group. A second active agent comprising a sequence consisting of at least three contiguous amino acids of groups R2-R8 in the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala, Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also described. The inventions are particularly useful in cell culture mediums. These cells may be used in transplantation techniques for treatment of malignant or inherited diseases. The formulae represent analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII), or AII AT2 type 2 receptor agonists.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
| | | | |  
Db 1 drvyyihp 7

# RESULT 4

AAW71113  
ID AAW71113 standard; peptide; 7 AA.

XX AC AAW71113;

XX DT 27-OCT-1998 (first entry)

XX DE Peptide AII(1-7) used to accelerate thermal wound healing.

XX KW Angiotensin; AII; acceleration; thermal wound healing; human;  
XX KW growth factor release; neovascularisation; re-epithelialisation;  
XX KW extracellular matrix production.

XX OS Synthetic.

XX PN W09833813-A2.

XX 06-AUG-1998.

XX PF 04-FEB-1998; 98WO-US02049.

XX PR 04-FEB-1997; 97US-0037166.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX DR WPI; 1998-437391/37.

XX PT Methods for accelerating thermal wound healing in humans - using  
XX PT angiotensinogen II and AII analogues

XX PS Claim 3; Page 9; 58pp; English.

XX CC AAW71110-27 represent peptide used in the method of the invention. The  
XX CC specification describes a method of accelerating thermal wound healing  
XX CC in humans. The method comprises applying to the thermally injured tissue  
XX CC an amount of at least one active agent which comprises the peptides  
XX CC AAW7115-27. The method can be used to promote the healing of thermal  
XX CC wounds by accelerating growth factor release, neovascularisation,  
XX CC re-epithelialisation and extracellular matrix production. The sequences  
XX CC are analogues of the angiotensin or angiotensinogen family of proteins.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
| | | | |  
Db 1 drvyyihp 7

# RESULT 5

AAAY49589  
ID AAY49589 standard; peptide; 7 AA.

XX AC AAY49589;

XX DT 13-JAN-2000 (first entry)

XX DE Angiotensin analogue peptide\_SEQ ID NO:4.

XX KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;  
XX KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.

XX OS Synthetic.

XX PN W09952540-A1.

XX PD 21-OCT-1999.

XX PF 07-APR-1999; 99WO-US07654.

XX PR 09-APR-1998; 98US-0081262.

XX PR 12-JUN-1998; 98US-0089024.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers KE, Dizerega G;

XX DR WPI; 1999-620285/53.

XX PT Treating or preventing infections in mammals using peptides derived  
XX PT from angiotensin or angiotensin receptor agonists

XX PS Claim 2; Page 10; 91pp; English.

XX CC The present invention describes a method for treating or preventing  
XX CC infections in mammals by administering peptides (A) that are fragments  
XX CC or analogues (or their fragments) of angiotensinogen, angiotensins I or  
XX CC II, or angiotensin II AT2-type receptor agonists. (A) contain at least  
XX CC 3 consecutive amino acids (aa) from the sequence (S1):

XX CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;  
XX CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane  
XX CC carboxylic acid), Ala, dimethylglycine, pro, betaine, Glu(NH2), Gly,  
XX CC Asp(NH2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,  
XX CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,  
XX CC Ile, Gly, Pro, Alb (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr  
XX CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;  
XX CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;  
XX CC R7 = pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =  
XX CC sequences having R4 as a terminal Tyr residue are excluded. The method  
XX CC is particularly used in cases of bacterial infection (e.g. septic shock,  
XX CC peritonitis, bacteraemia or endotoxaemia) but also against viral and  
XX CC parasitic infections. AAY49586 to AAY49623 represent specifically  
XX CC claimed examples of (A).

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||||

Db 1 drvyihp 7

## RESULT 6

AA50296

ID AAY50296 standard; Peptide; 7 AA.

XX

AC AAY50296;

XX

DT 12-JAN-2000 (first entry)

XX

DE Neutrophil-activating pancreatic derived peptide 96.

XX

KW Cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease; autoimmune diseases; arthritis; diabetes; stroke; organ rejection; ischemia; Alzheimer's disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.

XX

OS Unidentified.

XX

PN WO9946367-A2.

XX

PD 16-SEP-1999.

XX

PF 11-MAR-1999; 99WO-US05247.

XX

PR 11-MAR-1998; 98US-0038894.

XX

PA (CELL-) CELL ACTIVATION INC.

PA (REGC ) UNIV CALIFORNIA.

XX

PA (SCRI ) SCRIPPS RES INST.

XX

PI Stoughton RB, Schmid-Schonbein GW, Hugli TE, Kistler E;

XX

DR WPI; 1999-580234/49.

XX

PT Use of cell activating compositions in developing products for

PT diagnosis and treatment of e.g. cardiovascular, inflammatory,

PT autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,

PT diabetes, stroke or ischemia

XX

PS Example 9; Page 184; 184pp; English.

CC This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating composition comprising (a) homogenizing pancreatic tissue in buffer at about neutral or higher pH to produce a homogenate; (b) removing particulates from the homogenate; (c) optionally incubating the resulting homogenate, with particulates removed, with a protease; and (d) fractionating the homogenate and selecting fractions that exhibit cell activation activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular disease, inflammatory disease, trauma, autoimmune diseases, arthritis, organ rejection, diabetes and diabetic complications, stroke, ischemia, Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic retinopathy, diabetes, venous insufficiency, unstable angina or trauma. They can be used in the veterinary treatment of a non-human subject. Protease inhibitors can be used to lower cell activation resulting from these diseases and deficiencies. The detection of an elevated level of hydrogen peroxide can be used to detect an inflammatory condition. An elevated level of hydrogen peroxide in plasma or whole blood and in the presence of superoxide dismutase (SOD) indicates leukocyte up regulation, e.g. indicative of the onset of an acute cardiovascular disorders, such as disease onset or ischemic complications. An elevated level of hydrogen peroxide in plasma or whole blood and a low level in the presence of SOD is indicative of a chronic or immune compromised condition e.g. hypertension or sepsis. AAY50201-Y50334 represent peptides used in the method of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7

Db 1 drvyihp 7

## RESULT 7

AA53904

ID AAY33904 standard; peptide; 7 AA.

XX

AC AAY33904;

XX

DT 29-NOV-1999 (first entry)

XX

DE Angiotensin II analogue AII(1-7).

XX

KW embryonic stem cell; ES; angiotensin; totipotent cell;

KW gene therapy; replacement therapy; angiotensin II; AII;

KW analogue.

XX

OS Homo sapiens.

XX

PN WO9942122-A1.

XX

PD 26-AUG-1999.

XX

PF 16-FEB-1999; 99WO-US03243.

XX

PR 19-FEB-1998; 98US-0075179.

XX

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX

PI Dizerega G, Rodgers KE;

XX

DR WPI; 1999-527419/44.

XX

PT Promoting embryonal cell proliferation, using angiotensinogen and

PT angiotensin peptides, analogs or fragments

XX

PS Claim 2; Page 8; 76pp; English.

XX

CC This is the amino acid sequence of the Angiotensin II analogue,

CC AII(1-7). The formation of Angiotensin II (AII) is initiated by the

CC action of renin on the plasma substrate angiotensinogen.

CC This results in Angiotensin I (AI) which then converted to AII by the

CC converting enzyme angiotensinase which removes the C-terminal His-Leu

CC residues from AI (AAY42372).

CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and

CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,

CC or AII AT2 type 2 receptor agonists can rapidly provide a large

CC population of ESCs (Embryonic Stem Cell) for use in replacement therapy.

CC Similarly, methods that increase in vivo proliferation of ESCs will

CC enhance the utility of replacement therapy by rapidly increasing local

CC concentration of the stem cells and their progeny at the site of

CC therapy. The method also increases the potential utility of ESCs as

CC vehicles for gene therapy in certain disorders by more efficiently

CC providing a large number of such cells for transfection, and also by

CC providing a more efficient means to rapidly expand transected ESCs.

XX

Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 drvyihp 7

RESULT 8  
AAY30542  
ID AAY30542 standard; peptide; 7 AA.

AC AAY30542;  
XX  
DT 18-NOV-1999 (first entry)

XX Amino acid sequence of angiotensin II fragment AIII-7.

XX Angiotensin; analogue; tissue equivalent; cell proliferation.

XX Synthetic.

XX WO9946285-A2.

XX 16-SEP-1999.

XX PF 11-MAR-1999; 99WO-US05261.

XX PR 11-MAR-1998; 98US-0077499.

XX PR 12-JUN-1998; 98US-0089064.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Rodgers KE, Dizerega G;

XX DR WPI; 1999-551360/46.

XX An improved method for producing a tissue equivalent with angiotensin I  
PT and II derived active agents -

PS Claim 2; Page 52; 83pp; English.

XX AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII  
CC fragments and AII analogues. The peptides are used in the method  
CC of the invention. The specification describes an improved method  
CC for producing a tissue equivalent. The method comprises contacting  
CC the tissue equivalent with angiotensin I and II derived active  
CC agents. The methods are used for production and culture of tissue  
CC equivalents (three-dimensional cell and tissue culture systems),  
CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,  
CC vascular graft, cartilage, ligament, collagen lattice, liver and  
CC kidney tissue equivalents. The methods and tissue culture systems  
CC are used for the long-term proliferation of cells and tissues  
CC in an in vitro environment that more closely approximates that found  
CC in vivo.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 drvyihp 7

RESULT 9  
AAY30586  
ID AAY30586 standard; peptide; 7 AA.

AC AAY30586;

XX 18-NOV-1999 (first entry)

XX

DE Amino acid sequence of an angiotensin II (AII) fragment AIII-7.  
XX  
KW Angiotensin; analogue; radiation mitigation; tissue damage;  
KW radiation therapy; bone marrow transplantation; cancer therapy;  
KW megakaryocyte production; platelet production; hematopoietic disorder.

XX Synthetic.

XX WO9945945-A1.

XX 16-SEP-1999.

XX PF 08-MAR-1999; 99WO-US05194.

XX PR 10-MAR-1998; 98US-0077382.

XX PR 09-APR-1998; 98US-0081262.

XX PR 30-APR-1998; 98US-0083670.

XX PR 19-JUN-1998; 98US-0090096.

XX PR 22-JUN-1998; 98US-0090216.

XX PR 11-SEP-1998; 98US-0099957.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PA (RODG/) RODGERS K E.

XX PA (DIZE/) DIZEREGA G.

XX PI Rodgers KE, Dizerega G;

XX DR WPI; 1999-551209/46.

XX Claim 2; Page 85; 116pp; English.

XX AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII  
CC fragments and AII analogues. The peptides are used in the method  
CC of the invention. The specification describes a method for mitigating  
CC radiation induced tissue damage, improving the effectiveness of  
CC radiation therapy, to support bone marrow transplantation, and  
CC promoting megakaryocyte production and mobilization and platelet  
CC production. The method comprises administration of the present peptides.  
CC The methods can be used to mitigate radiation induced tissue damage, to  
CC improve the effectiveness of radiation therapy, to support bone marrow  
CC transplantation, and to promote megakaryocyte production and  
CC mobilization and platelet production. They are used particularly in  
CC cancer therapy. They can also be used to provide megakaryocytes as  
CC vehicles for gene therapy in hematopoietic disorders, by providing a  
CC more efficient means to rapidly expand transduced megakaryocytes.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 drvyihp 7

RESULT 10  
AAY32717  
ID AAY32717 standard; peptide; 7 AA.

AC AAY32717;

XX 09-NOV-1999 (first entry)

XX Angiotensin II analogue AII(1-7).

KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;  
 KW chemotaxis; growth factor; liver regeneration; cirrhosis;  
 KW hepatocarcinoma; hepatectomy; transplantation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN WO9939743-A2.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 08-FEB-1999; 99WO-US02618.  
 XX  
 XX 13-NOV-1998; 98US-0108412.  
 PR 09-FEB-1998; 98US-0074104.  
 XX  
 XX (DIZE/) DIZEREGA G.  
 PA (RODG/) RODGERS K E.  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 DR WPI; 1999-508461/42.  
 XX  
 XX Hepatic cell proliferation with angiotensin I and II derived active  
 PT agents, useful for regeneration of liver after resection  
 PT  
 XX Claim 2; Page 9; 66pp; English.  
 PS  
 XX Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The  
 CC peptides are derived from the AII peptide (AAY32750). AII increases  
 CC mitogenesis and chemotaxis in cultured cells, and also increases the  
 CC release of growth factors and extracellular matrices. AII has also been  
 CC shown to increase the proliferation of certain cell types. The AII  
 CC analogue peptides can be used as the active agent in a method for  
 CC promoting hepatic cell proliferation and differentiation. The method  
 CC involves contacting the hepatic cells with an amount effective enough to  
 CC promote proliferation of any of the peptides. This method is useful in  
 CC liver regeneration following resection of hepatocarcinomas, hepatitis  
 CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic  
 CC failure, hepatocyte transplantation, liver transplantation and other  
 CC hepatic disorders where rapid regeneration of the liver is desirable. The  
 CC methods are also useful in rapidly providing a large population of  
 CC hepatic cells for use in cell therapy and for providing a large  
 CC population of transfectant hepatic cells for use in gene therapy.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7  
 | | | | | | |  
 Db 1 drvylhp 7

RESULT 11  
 AAY33771  
 ID AAY33771 standard; peptide; 7 AA.  
 XX  
 AC AAY33771;  
 XX  
 XX 09-NOV-1999 (first entry)  
 DT  
 XX Angiotensin II (AII) octapeptide fragment AII(1-7).  
 DE  
 XX Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;  
 KW neuronal cell proliferation; differentiation; Alzheimer's disease;  
 KW Parkinson's disease; neuron replacement therapy.  
 XX  
 OS Homo sapiens.

XX WO9942123-A1.  
 PN  
 XX 26-AUG-1999.  
 PD  
 XX 19-FEB-1999; 99WO-US03772.  
 PF  
 XX 19-FEB-1998; 98US-0075232.  
 PR  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PA  
 XX Dizerega G, Rodgers KE;  
 PI WPI; 1999-527420/44.  
 DR  
 XX Promoting neuronal cell proliferation and differentiation  
 PT  
 XX Claim 2; Page 10; 62pp; English.  
 PS  
 XX Sequences AAY3769-Y33802 are fragments or analogues of the angiotensin  
 CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The  
 CC application of angiotensin to wound tissue significantly increases the  
 CC rate of wound healing. AII is known to increase mitogenesis and  
 CC chemotaxis in cultured cells, and also increases their release of growth  
 CC factors and extracellular matrices, implicating it in cell growth and  
 CC differentiation. AT2 receptors are receptors for AII and are thought to  
 CC be involved in the mediation of the cell differentiation effects of AII.  
 CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal  
 CC cell proliferation or differentiation. This method is useful in the  
 CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement  
 CC therapy.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7  
 | | | | | | |  
 Db 1 drvylhp 7

RESULT 12  
 AAY15348  
 ID AAY15348 standard; peptide; 7 AA.  
 XX  
 AC AAY15348;  
 XX  
 XX 09-NOV-1999 (first entry)  
 DT  
 XX Angiotensin II (AII) analogue, AII(1-7).  
 DE  
 XX burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;  
 KW AII; analogue; chronic renal failure; cancer; bone marrow.  
 KW  
 XX Synthetic.  
 OS  
 OS Homo sapiens.  
 XX  
 XX WO9940106-A2.  
 PN  
 XX 12-AUG-1999.  
 PD  
 XX 08-FEB-1999; 99WO-US02648.  
 PF  
 XX 09-DEC-1998; 98US-0111535.  
 PR 09-FEB-1998; 98US-0074106.  
 PR  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PA  
 XX Dizerega G, Rodgers KE;  
 PI  
 XX



DR WPI; 1999-508486/42.  
XX Promoting erythropoiesis with angiotensin I and II derived active  
PT agents, useful for treatment of, e.g. congenital or acquired  
PT aplastic or hypoplastic anemia  
XX  
XX Claim 2; Page 9; 76pp; English.  
XX  
XX This sequence is an angiotensin II (AII) analogue. Similar sequences  
CC also based on the AII peptide have been tested against each other, AII  
CC and a negative control. These active agents have been shown to affect  
CC the levels of BFU-E (burst forming units-erythroid) in culture.  
CC The active agents (AAV15348, AAV15359, AAV15372, AAV15379, and AAV15380)  
CC augment erythropoiesis by potentiating erythropoietin-induced  
CC differentiation. Increasing the rate of erythropoiesis improves clinical  
CC benefits for the treatment of congenital or acquired aplastic or  
CC hypoplastic anemia associated with chronic renal failure, end-stage renal  
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,  
CC bone marrow transplantation and chronic diseases.  
CC The active agents permit the use of smaller doses of erythropoietin  
CC therefore decreasing treatment costs.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 drvyihp 7  
|||||

## RESULT 13

AAV15308  
ID AAV15308 standard; peptide; 7 AA.  
XX  
AC AAV15308;  
XX  
DT 09-NOV-1999 (first entry)  
XX  
DE Angiotensin II (AII) analogue, AII(1-7).  
XX  
KW angiotensin; angiotensin II; AII; wound healing; scarring;  
KW tissue repair; agonist; analogue.

XX Synthetic.  
XX Homo sapiens.

PN W09940107-A2.  
XX  
PD 12-AUG-1999.  
XX  
XX 08-FEB-1999; 99WO-US02725.  
XX  
XX 09-FEB-1998; 98US-0074105.  
XX  
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

DR WPI; 1999-508487/42.

XX Epithelial stem cell and keratinocyte proliferation with angiotensin  
PT I and II derived active agents, useful for treatment of skin wounds  
XX  
XX Claim 2; Page 10; 70pp; English.

XX This is the amino acid sequence of an Angiotensin II analogue. This and  
CC other similar analogues (AAV15306 to AAV15316 and AAV15321 to AAV15337)  
CC can be used to promote the proliferation of epithelial stem cells and  
CC Keratinocytes leading to a more rapid and efficient cellular response to

CC stratified epithelial injury. The angiotensin analogues are derived from  
CC an octapeptide present in humans and other species which has the  
CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAV15342) and is known as  
CC angiotensin II (AII). This is formed by the action of renin on the  
CC plasma substrate called angiotensinogen, the product of this reaction is a  
CC decapeptide called angiotensin I (AI) which is converted to AII by the  
CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
CC residues from AI (AAV15339).

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 drvyihp 7  
|||||

## RESULT 14

AAV26205  
ID AAB26205 standard; peptide; 7 AA.

XX  
AC AAB26205;

XX  
DT 23-FEB-2001 (first entry)

XX Anion exchange resin EPM-1 test peptide #1.

XX Anion exchange resin; ionic solute separation;  
KW column liquid chromatography; EPM-1.

XX Synthetic.

XX Key Location/Qualifiers  
FT Modified-site 7  
FT /label= OTHER  
FT /note= "modified by CONH2"

XX W0200050465-A2.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-BR00023.

XX 24-FEB-1999; 99BR-0004682.

XX (CNPQ-) CNPQ CONSELHO NACIONAL DESENVOLVIMENTO.

XX Ryuichi Nakate C, Cilli EM, Jabilut GN, Haddad Carvalho RS;

XX WPI; 2000-572075/53.

XX New crosslinked polystyrene containing aminomethyl groups, useful as  
PT ion-exchange resin, particularly for separation of biomolecules from  
PT electrophoretic gel

XX Disclosure; Page 4; 17pp; English.

XX The present sequence is a peptide used as a test for the novel anion  
CC exchange resin aminomethyl-resin (EPM-1). The peptide has a charge of  
CC plus 2 and so acts as a control for the occurrence of unspecific  
CC interactions in the EPM-1 matrix. The EPM-1 resin can be used in column  
CC liquid chromatography, in particular for the separation of ionic solutes.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
| | | | |  
Db 1 drvyihp 7

RESULT 15  
AAB27404  
ID AAB27404 standard; Peptide; 7 AA.  
XX  
AC AAB27404;  
XX  
DT 23-JAN-2001 (first entry)  
XX  
DE Angiotensin II analog AII(1-7).  
XX  
KW Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;  
KW cardiomyopathies; inflammation; infection; sepsis; ischemia;  
KW heart valve disease; myocarditis; angiotensin.  
Synthetic.

XX  
PN WO200053211-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-US06198.  
XX  
PR 09-MAR-1999; 99US-0123678.  
PR 31-AUG-1999; 99US-0151874.  
XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX  
PI Rodgers K, Dizerega G;  
XX  
DR WPI; 2000-611400/58.  
XX  
PT Promoting myocyte proliferation and myocardial tissue repair by  
PT contacting myocytes with angiotensinogen or angiotensin I or II, useful  
PT for treating heart attacks, cardiomyopathies, inflammation and  
PT infection -  
XX  
PS Claim 2; Page 10; 55pp; English.  
XX

XX  
CC The present invention relates to a method of promoting myocyte  
CC proliferation or differentiation by contacting myocytes with an active  
CC agent containing angiotensinogen, angiotensin I and II (AI, AII), and  
CC angiotensin analogs. The present sequence is an angiotensin II analog  
CC of the invention. The active agents of the invention may be useful for  
CC promoting myocardial tissue repair following myocardial injury and for  
CC treating heart failure in a mammal. Administration to accelerate in  
CC vivo myocyte proliferation and/or to treat myocardial injuries can be  
CC used to treat cardiomyopathies, inflammation, infection, sepsis,  
CC ischemia, heart valve disease, myocarditis, inflammation, myocardial  
CC ischemia and infarction and for improving cardiac output by increasing  
CC stroke volume.  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
| | | | |  
Db 1 drvyihp 7

Search completed: July 1, 2002, 07:41:54  
Job time: 346 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:37:59 ; Search time 59.1 Seconds  
(without alignments)  
2.893 Million cell updates/sec

Title: US-09-723-197-4  
Perfect score: 41  
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCrUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	7	2	US-08-465-775-4
2	41	100.0	7	3	US-09-208-337-4
3	41	100.0	7	3	US-08-990-664-5
4	41	100.0	7	4	US-09-373-962-4
5	41	100.0	7	4	US-09-245-680-4
6	41	100.0	7	4	US-09-198-806C-4
7	41	100.0	7	4	US-09-352-191-4
8	41	100.0	7	4	US-09-012-400-4
9	41	100.0	7	6	5451571-4
10	41	100.0	8	1	US-07-858-842-2
11	41	100.0	8	1	US-08-021-839A-3
12	41	100.0	8	1	US-08-184-935-2
13	41	100.0	8	1	US-08-212-433A-29
14	41	100.0	8	1	US-08-185-448-8
15	41	100.0	8	1	US-07-776-272-1
16	41	100.0	8	1	US-08-428-488-21
17	41	100.0	8	1	US-08-337-781-1
18	41	100.0	8	1	US-08-240-711-20
19	41	100.0	8	1	US-08-594-117-1
20	41	100.0	8	1	US-08-520-770-2
21	41	100.0	8	1	US-08-457-753-20
22	41	100.0	8	2	US-08-115-968-1
23	41	100.0	8	2	US-08-115-968-3
24	41	100.0	8	2	US-08-115-968-4
25	41	100.0	8	2	US-08-465-774-1
26	41	100.0	8	2	US-08-360-784B-2
27	41	100.0	8	2	US-08-623-833B-4

28	41	100.0	8	2	US-08-465-775-1	Sequence 1, Appli
29	41	100.0	8	2	US-08-542-927-3	Sequence 3, Appli
30	41	100.0	8	3	US-07-116-256-29	Sequence 29, Appl
31	41	100.0	8	3	US-09-054-308A-2	Sequence 2, Appli
32	41	100.0	8	3	US-09-280-047-7	Sequence 7, Appli
33	41	100.0	8	3	US-09-208-337-1	Sequence 1, Appli
34	41	100.0	8	3	US-08-990-664-1	Sequence 30, Appl
35	41	100.0	8	3	US-08-990-664-30	Sequence 16, Appl
36	41	100.0	8	4	US-08-927-128-16	Sequence 1, Appli
37	41	100.0	8	4	US-09-210-249-1	Sequence 8, Appli
38	41	100.0	8	4	US-09-210-249-8	Sequence 1, Appli
39	41	100.0	8	4	US-09-373-962-1	Sequence 29, Appl
40	41	100.0	8	4	US-09-373-962-29	Sequence 32, Appl
41	41	100.0	8	4	US-09-373-962-32	Sequence 42, Appl
42	41	100.0	8	4	US-09-373-962-42	Sequence 25, Appl
43	41	100.0	8	4	US-09-289-693-25	Sequence 1, Appli
44	41	100.0	8	4	US-09-245-680-1	Sequence 29, Appl
45	41	100.0	8	4	US-09-245-680-2	

ALIGNMENTS

RESULT 1  
US-08-465-775-4  
; Sequence 4, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: gizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-775-4

Query Match 100.0%; Score 41; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
DB 1 DRVYIHP 7

RESULT 2  
US-09-208-337-4  
; Sequence 4, Application US/09208337  
; Patent No. 6096709  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: Gere, dizerega  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,337  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,775  
; FILING DATE: 06-JUN-1995  
; APPLICATION NUMBER: 08/337,781  
; FILING DATE: 14-NOV-1994  
; APPLICATION NUMBER: 08/126,368  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC010.001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 949-760-0404  
; TELEFAX: 949-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-09-208-337-4

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7  
| | | | |  
Db 1 DRVYIHP 7

RESULT 3  
US-08-990-664-5  
; Sequence 5, Application US/08990664  
; Patent No. 6110895  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
; TITLE OF INVENTION: IN SKIN GRAFTS  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/990,664  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/028,310  
; FILING DATE: 16-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC012.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-760-0404  
; TELEFAX: 714-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-990-664-5

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7  
| | | | |  
Db 1 DRVYIHP 7

RESULT 4  
US-09-373-962-4  
; Sequence 4, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-373-962-4

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7  
| | | | |  
Db 1 DRVYIHP 7

RESULT 5  
US-09-245-680-4  
; Sequence 4, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245.680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-245-680-4

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 DRVYIHP 7

RESULT 6  
US-09-198-806C-4  
; Sequence 4, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-198-806C-4

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 DRVYIHP 7

RESULT 7  
US-09-352-191-4  
; Sequence 4, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue

; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352,191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-352-191-4

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 DRVYIHP 7

RESULT 8  
US-09-012-400-4  
; Sequence 4, Application US/09012400D  
; Patent No. 6335195  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell  
; TITLE OF INVENTION: Proliferation and Differentiation  
; FILE REFERENCE: 97,017-G  
; CURRENT APPLICATION NUMBER: US/09/012,400D  
; CURRENT FILING DATE: 1998-01-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-7)  
US-09-012-400-4

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
Db 1 DRVYIHP 7

RESULT 9  
5451571-4  
; Patent No. 5451571  
; APPLICANT: FERRARIO, CARLOS M.; SANTOS, ROBSON A.S.;  
; BROSNIHAN, KAY B.  
; TITLE OF INVENTION: PROCESS AND COMPOSITION FOR TREATING  
; HYPERTENSION  
; NUMBER OF SEQUENCES: 5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/345,547  
; FILING DATE: 28-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 845,778  
; FILING DATE: 04-MAR-1992  
; APPLICATION NUMBER: 613,955  
; FILING DATE: 13-NOV-1990  
; APPLICATION NUMBER: 259,929

Query Match 100.0%; Score 41; DB 6; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7

Db 1 DRVYIHP 7

RESULT 10

US-07-858-842-2

; Sequence 2, Application US/07858842

; Patent No. 5314807

; GENERAL INFORMATION:

; APPLICANT: Yoshikawa, Masaaki

; APPLICANT: Yokoyama, Keiichi

; APPLICANT: Hasegawa, Masayasu

; APPLICANT: Yasumoto, Ryouichi

; APPLICANT: Fujita, Hiroyuki

; TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARMSTRONG & KUBOVCIK

; STREET: 1725 K Street N.W. Suite 1000

; CITY: Washington

; STATE: District of Columbia

; COUNTRY: United States of America

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/858,842

; FILING DATE: 19920327

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 142283

; FILING DATE: 29-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 298060

; FILING DATE: 17-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Gormley, Mary E.

; REGISTRATION NUMBER: 34, 409

; REFERENCE/DOCKET NUMBER: 920247

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 659-2930

; TELEFAX: (202) 887-0357

; TELEX: 440142

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; US-07-858-842-2

Query Match

Best Local Similarity 100.0%; Score 41; DB 1; Length 8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7

Db 1 DRVYIHP 7

RESULT 11

US-08-021-839A-3

; Sequence 3, Application US/08021839A

; Patent No. 5326776

; GENERAL INFORMATION:

; APPLICANT: Winn, Martin

; APPLICANT: De, Biswanath

; APPLICANT: Zydowsky, Thomas M.

; APPLICANT: Kerkman, Daniel J.

; APPLICANT: Debernardis, John F.

; APPLICANT: Rosenberg, Saul H.

; APPLICANT: Shiosaki, Kazumi

; APPLICANT: Basha, Fatima Z.

; APPLICANT: Spina, Kenneth P.

; APPLICANT: Von Geldern, Thomas W.

; TITLE OF INVENTION: Angiotensin II Receptor Antagonists

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edward H. Gorman, Jr.

; STREET: Abbott Laboratories

; STREET: D-377/AP6D

; STREET: One Abbott Park Road

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb

; COMPUTER: Apple Macintosh IIci

; OPERATING SYSTEM: Macintosh

; SOFTWARE: Microsoft Word 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/021,839A

; FILING DATE: 24-FEB-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/844,817

; FILING DATE: 02-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Steven R. Crowley

; REGISTRATION NUMBER: 31,604

; REFERENCE/DOCKET NUMBER: 5136.US.PI

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (708) 938-7742

; TELEFAX: (708) 938-2623

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acid residues

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; DESCRIPTION: peptide

; US-08-021-839A-3

Query Match

Best Local Similarity 100.0%; Score 41; DB 1; Length 8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7

Db 1 DRVYIHP 7

RESULT 12

US-08-184-935-2

; Sequence 2, Application US/08184935

; Patent No. 5476770  
; GENERAL INFORMATION:  
; APPLICANT: PRADIELLES, PHILIPPE  
; TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN  
; TITLE OF INVENTION: OR HAPTEN  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; City: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/184,935  
; FILING DATE: 24-JAN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5476770man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 846-286-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-184-935-2

Query Match 100.0%; Score 41; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRVYIHP 7  
Db 1 DRVYIHP 7

SULT 13  
US-08-212-433A-29  
; Sequence 29 Application US/08212433A  
; Patent No. 5538897  
; GENERAL INFORMATION:  
; APPLICANT: Yates, III, John R.  
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION  
; TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN  
; TITLE OF INVENTION: DATABASES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: One Market Plaza, Stewart St. Tower  
; City: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/212.433A  
; FILING DATE: 14-MAR-1994  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hughes, Richard L.  
; REGISTRATION NUMBER: 31,264  
; REFERENCE/DOCKET NUMBER: 16336-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-467-9600  
; TELEFAX: 415-543-5043  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-212-433A-29

Query Match 100.0%; Score 41; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRVYIHP 7  
Db 1 DRVYIHP 7

RESULT 14  
US-08-185-448-8  
; Sequence 8, Application US/08185448  
; Patent No. 5580747  
; GENERAL INFORMATION:  
; APPLICANT: SHULTZ, JOHN W.  
; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,  
; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL  
; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100  
; City: MILWAUKEE  
; STATE: WISCONSIN  
; COUNTRY: USA  
; ZIP: 53202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/185.448  
; FILING DATE: 21-JAN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,928  
; FILING DATE: 12-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SARA, CHARLES S  
; REGISTRATION NUMBER: 30492  
; REFERENCE/DOCKET NUMBER: F.3347-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 255-2022  
; TELEFAX: (608) 255-2182  
; TELEX: 26832 ANDSTARK  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

Job time: 301 sec

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; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1
; OTHER INFORMATION: /label= LABEL
; OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
; OTHER INFORMATION: DETECTION TAG"
;
US-08-185-448-8
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Query Match 100.0%; Score 41; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
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|  
|  
|  
Db 1 DRVYIHP 7

```

RESULT 15
07-776-272-1
Sequence 1, Application US/07776272
Patent No. 5612454
GENERAL INFORMATION:
APPLICANT: Kaminuma, Toshihiko
APPLICANT: Iida, Toshi
APPLICANT: Tajima, Masahiro
TITLE OF INVENTION: Process for Purification of Polypeptide
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wegner, Cantor, Mueller & Player
STREET: 1233 20th St. N.W. P.O. Box 18218
CITY: Washington
STATE: District of Columbia
COUNTRY: United States of America
ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/776,272
FILING DATE: 19911129
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-23167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-0400
TELEFAX: 202-887-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOPHETICAL: YES
US-07-776-272-1
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Query Match 100.0%; Score 41; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
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|  
|  
Db 1 DRVYIHP 7



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:38:24 ; Search time 122.73 seconds  
(without alignments)  
9.867 Million cell updates/sec

Title: US-09-723-197-4  
Perfect score: 41  
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	100.0	14	5	Q10757 theromyzon
2	41	100.0	245	6	Q95J13 pan troglod
3	41	100.0	295	4	Q9HA44 homo sapien
4	41	100.0	461	11	Q9D2V0 Q9d2v0 mus muscullu
5	41	100.0	477	4	Q96FD5 Q96fd5 homo sapien
6	41	100.0	485	4	Q96F91 Q96f91 homo sapien
7	41	100.0	485	6	Q9GLP7 Q9glp7 pan troglod
8	41	100.0	485	6	Q9GLP6 Q9glp6 gorilla gor
9	41	100.0	485	6	Q9GLN8 Q9gln8 pan troglod
10	41	100.0	486	6	Q9TSZ0 Q9tsz0 callithrix
11	40	97.6	10	13	Q9PS07 Q9ps07 alligator m
12	38	92.7	171	17	Q97IG2 Q97lg2 sulfolobus
13	36	87.8	277	10	Q80539 Q80539 arabidopsis
14	36	87.8	280	10	Q940A3 Q940a3 arabidopsis
15	36	87.8	289	10	Q9FVU1 Q9fvul arabidopsis
16	35	85.4	436	11	Q9CSJ0 Q9csj0 mus muscullu

17	35	85.4	533	4	Q96SF7	Q96sf7 homo sapien
18	35	85.4	694	2	Q9EWA5	Q9ewa5 streptomyce
19	35	85.4	1094	2	Q93H78	Q93h78 streptomyce
20	35	85.4	1147	5	Q9Y1H3	Q9y1h3 dictyosteli
21	34	82.9	128	16	Q9K1A7	Q9kia7 neisseria m
22	34	82.9	132	16	Q9PG09	Q9pg09 xylella fas
23	34	82.9	149	2	Q57032	Q57032 synecocyst
24	34	82.9	168	8	O48244	O48244 dennys car
25	34	82.9	168	8	O48245	O48245 dennys car
26	34	82.9	175	5	O9GQE4	O9gqe4 branchiosto
27	34	82.9	183	5	O9GQE6	O9gqe6 branchiosto
28	34	82.9	316	2	Q9Z5B8	Q9z5b8 streptomyce
29	34	82.9	380	8	Q9GOM4	Q9gom4 arapaima gi
30	34	82.9	624	5	Q966R5	Q966r5 branchiosto
31	34	82.9	883	5	Q9VX1	Q9vx1 drosophila
32	33	80.5	56	16	Q9PCT3	Q9pct3 xylella fas
33	33	80.5	87	10	Q93YLO	Q93ym0 brassica ju
34	33	80.5	88	10	Q93YM2	Q93ym2 brassica ju
35	33	80.5	221	10	Q9ZVR9	Q9zvr9 arabidopsis
36	33	80.5	237	4	Q9H5S9	Q9h5s9 homo sapien
37	33	80.5	249	13	Q9W7O1	Q9w7q1 paralichthy
38	33	80.5	275	4	Q9BTA8	Q9bta8 homo sapien
39	33	80.5	288	2	Q55040	Q55040 synecococc
40	33	80.5	380	8	Q955N7	Q955n7 siphateles
41	33	80.5	394	5	P91817	P91817 tachypleus
42	33	80.5	437	13	Q9DDU4	Q9ddu4 brachydanio
43	33	80.5	457	6	Q9XSH5	Q9xsh5 salmire bol
44	33	80.5	695	5	Q9XUQ0	Q9xuo0 caenorhabdi
45	33	80.5	736	10	Q9LMH6	Q9lmh6 arabidopsis

#### ALIGNMENTS

RESULT 1

ID Q10757 PRELIMINARY; PRT; 14 AA.  
AC Q10757;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE ANGIOTENSINOGEN (FRAGMENT).  
OS Theromyzon tessulatum (Leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
OX NCBI\_TaxID=13286;  
RN [1]  
RX MEDLINE=95365039; PubMed=7637887;  
RA Laurent V., Bulet P., Salzet M.A.;  
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like molecule with forms of vertebrate angiotensinogens: a hormonal system conserved in the course of evolution.";  
RL Neurosci. Lett. 190:175-178(1995).  
RN [2]  
RP SEQUENCE OF 1-10.  
RC TISSUE=BRAIN;  
RX MEDLINE=96201949; PubMed=8612806;  
RA Laurent V., Salzet M.;  
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon tessulatum.";  
RL FEBS Lett. 384:123-127(1996).  
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.  
KW Glycoprotein; Serpin.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEFBD7 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.071;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7

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Db 1 DRVYIHP 7
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RESULT 2
Q95J13 PRELIMINARY; PRT; 245 AA.
AC Q95J13;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
GN REN.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504, AND 505;
DE Satta Y.;
DE "Comparison of DNA and protein polymorphisms between humans and
DE chimpanzees";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062027; BAB55856.1; -
DR EMBL; AB062028; BAB55857.1; -
FT NON_TER 245
SQ SEQUENCE 245 AA; 26317 MW; E0092390B9803E0B CRC64;

Query Match 100.0%; Score 41; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. NO. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||
Db 34 DRVYIHP 40

RESULT 3
Q9HA44 PRELIMINARY; PRT; 295 AA.
AC Q9HA44;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE TRANSCRIPTION FACTOR TBX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022330; BAB14014.1; -
DR HSSP; P24781; IYBR.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS02525; TBOX_3; 1.
SQ SEQUENCE 295 AA; 33197 MW; F2BD3E53E0ED21E0 CRC64;

Query Match 100.0%; Score 41; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. NO. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||
Db 170 DRVYIHP 176

RESULT 4
Q9D2V0 PRELIMINARY; PRT; 461 AA.
AC Q9D2V0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN AGT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
DE MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK018763; BAB31393.1; -
DR MGD; MGI:87963; Agt.
DR InterPro; IPR000227; Angiotensngn.
DR DR InterPro; IPR000215; Serpin.
DR PRINTS; PR00654; ANGIOTENSNGN.
DR SMART; SM00093; SERPIN; 1.
SQ SEQUENCE 461 AA; 50327 MW; 446E0881079251F CRC64;

Query Match 100.0%; Score 41; DB 11; Length 461;
Best Local Similarity 100.0%; Pred. NO. 2.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||
Db 30 DRVYIHP 36

RESULT 5
Q96FD5 PRELIMINARY; PRT; 477 AA.
AC Q96FD5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
SQ SEQUENCE 477 AA; 50327 MW; 446E0881079251F CRC64;
```

DE SIMILAR TO ANGIOTENSINOGEN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN, AND GLOBLASTOMA WITH EGFR AMPLIFICATION;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011231; AAH11231.1; -.  
 SQ SEQUENCE 477 AA; 51985 MW; AB798B70592FDE2 CRC64;

Query Match 100.0%; Score 41; DB 4; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 DRVYIHP 7  
 |||||  
 Db 25 DRVYIHP 31

RESULT 6  
 Q96F91 PRELIMINARY; PRT; 485 AA.  
 AC Q96F91;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ANGIOTENSINOGEN (SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE  
 DE A (ALPHA-1 ANTITRYPSIN, ANTI-TRYPsin), MEMBER 8).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN, AND GLOBLASTOMA WITH EGFR AMPLIFICATION;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011519; AAH11519.1; -.  
 SQ SEQUENCE 485 AA; 53114 MW; 50BA5E9DCD4C8E7F CRC64;

Query Match 100.0%; Score 41; DB 4; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 2.8; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 DRVYIHP 7  
 |||||  
 Db 34 DRVYIHP 40

RESULT 7  
 Q9GLP7 PRELIMINARY; PRT; 485 AA.  
 AC Q9GLP7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ANGIOTENSINOGEN.  
 GN AGT.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shattuck-Eidens D., McGrail M., Stone S.;  
 RT "Germline mutations in the angiotensinogen gene cause predisposition  
 RT to type 1 diabetes mellitus."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR EMBL; AF188487; AAG29056.1; -.  
 DR InterPro; IPR000227; Angiotensngn.  
 DR InterPro; IPR000215; Serpin.  
 DR PRINTS; PR00654; ANGIOTENSNGN.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; 1.  
 KW Serpin.  
 SQ SEQUENCE 485 AA; 53140 MW; 49EFB54AF31F8ADC CRC64;

Query Match 100.0%; Score 41; DB 6; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 2.8; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 DRVYIHP 7  
 |||||  
 Db 34 DRVYIHP 40

RESULT 8  
 Q9GLP6 PRELIMINARY; PRT; 485 AA.  
 AC Q9GLP6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ANGIOTENSINOGEN.  
 GN AGT.  
 OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OX NCBI\_TaxID=9593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shattuck-Eidens D., McGrail M., Stone S.;  
 RT "Germline mutations in the angiotensinogen gene cause predisposition  
 RT to type 1 diabetes mellitus."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR EMBL; AF188488; AAG29057.1; -.  
 DR InterPro; IPR000227; Angiotensngn.  
 DR InterPro; IPR000215; Serpin.  
 DR PRINTS; PR00654; ANGIOTENSNGN.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; 1.  
 KW Serpin.  
 SQ SEQUENCE 485 AA; 53186 MW; 53BC9235271C8255 CRC64;

Query Match 100.0%; Score 41; DB 6; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 2.8; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 DRVYIHP 7  
 |||||  
 Db 34 DRVYIHP 40

RESULT 9  
 Q9GLN8 PRELIMINARY; PRT; 485 AA.  
 AC Q9GLN8;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ANGIOTENSINOGEN.  
 GN AGT.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE-20469400; PubMed=11013071;  
RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,  
RA Jeunemaitre X.;  
RT "Human-Chimpanzee DNA sequence variation in the four major genes of  
the renin angiotensin system.";  
RL Genomics 69:114-26(2000).  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AF193461; AAG30306.1; -.  
DR EMBL; AF193458; AAG30306.1; JOINED.  
DR EMBL; AF193459; AAG30306.1; JOINED.  
DR EMBL; AF193460; AAG30306.1; JOINED.  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR PRINTS; PR00654; ANGIOTENSNG.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
KW Serpin.  
SQ SEQUENCE 485 AA; 53110 MW; C14C67E49A53F05F CRC64;

Query Match 100.0%; Score 41; DB 6; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 34 DRVYIHP 40

RESULT 10  
Q9TSZ0  
ID Q9TSZ0 PRELIMINARY; PRT; 486 AA.  
AC Q9TSZ0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ANGIOTENSINOGEN PRECURSOR.  
GN ANGT.  
OS Callithrix jacchus (Common marmoset).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Callithrix.  
OX NCBI\_TaxID=9483;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-20065005; PubMed=10598135;  
RA Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;  
RT "Cloning and characterization of marmoset renin: comparison with human  
renin.";  
RL J. Cardiovasc. Pharmacol. 34:893-897(1999).  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; AJ132343; CAB64880.1; -.  
DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNG.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
KW Serpin; Signal.  
FT SIGNAL 1 33 POTENTIAL.  
FT CHAIN 34 486 ANGIOTENSINOGEN.  
SQ SEQUENCE 486 AA; 53374 MW; 5408129B2F71FB8B CRC64;

Query Match 100.0%; Score 41; DB 6; Length 486;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 34 DRVYIHP 40

RESULT 11  
Q9PS07  
ID Q9PS07 PRELIMINARY; PRT; 10 AA.  
AC Q9PS07;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE ANGIOTENSIN I, ANG I.  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE-93307610; PubMed=8319878;  
RA Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,  
RA Stephens G.A., Sakakibara S.;  
RT "New angiotensin I isolated from a reptile, Alligator  
mississippiensis.";  
RL Gen. Comp. Endocrinol. 90:214-219(1993).  
SQ SEQUENCE 10 AA; 1216 MW; CEE38DD761F2DB42 CRC64;

Query Match 97.6%; Score 40; DB 13; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.08;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 1 DRVYIHP 7

RESULT 12  
Q971G2  
ID Q971G2 PRELIMINARY; PRT; 171 AA.  
AC Q971G2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL PROTEIN ST1391.  
GN ST1391.  
OS Sulfolobus tokodaii.  
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
OX NCBI\_TaxID=111955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JCM 10545 / 7;  
RX PubMed=11572479;  
RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,  
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
RA Oshima T., Kikuchi H.;  
RT "Complete genome sequence of an aerobic thermoacidophilic  
Crenarchaeon, Sulfolobus tokodaii strain7.";  
RL DNA Res. 8:123-140(2001).  
DR EMBL; AF000986; BAB66458.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 171 AA; 18700 MW; 897F397EAD34EF0A CRC64;

Query Match 92.7%; Score 38; DB 17; Length 171;  
Best Local Similarity 85.7%; Pred. No. 3.9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 16 DRVYIHP 22

RESULT 13  
O80539

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ID O80539 PRELIMINARY; PRT; 277 AA.
AC O80539;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE F14J9.24 KDA PROTEIN.
DE F14J9.24.
GN F14J9.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
RA Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,
RA Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S.,
RA Yu G., Ecker J., Theologis A., Davis R.W.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RA EMBL: AC003970; AAC33217.1;
SQ SEQUENCE 277 AA; 31908 MW; EB65DCCA29C36D46 CRC64;

Query Match 87.8%; Score 36; DB 10; Length 277;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
Db 108 DKVYLHP 114
I:|:|:|

RESULT 14
Q940A3 PRELIMINARY; PRT; 280 AA.
AC Q940A3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE F14J9.24 KDA PROTEIN.
GN F14J9.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesena E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA "Full length cDNA of gene F14J9.24 (GI:3482932).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL: AY056149; AAL07228.1;
KW Hypothetical protein.
SQ SEQUENCE 280 AA; 32441 MW; 4252585A11002102 CRC64;

Query Match 87.8%; Score 36; DB 10; Length 280;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
Db 119 DKVYLHP 125
I:|:|:|
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RESULT 15
Q9FVU1 PRELIMINARY; PRT; 289 AA.
ID Q9FVU1;
AC Q9FVU1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE F14J9.24 KDA PROTEIN.
DE F14J9.24.
GN F14J9.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana.";
RL Nature 408:816-820(2000).
DR EMBL: AC079733; AAG50752.1;
KW Hypothetical protein.
SQ SEQUENCE 289 AA; 33181 MW; BE15FFAB7CD7C608 CRC64;

Query Match 87.8%; Score 36; DB 10; Length 289;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
Db 111 DKVYLHP 117
I:|:|:|
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Search completed: July 1, 2002, 07:45:10  
Job time: 406 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:38:59 ; Search time 69.93 seconds  
(without alignments)  
9.619 Million cell updates/sec

Title: US-09-723-197-4  
Perfect score: 41  
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR-71:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	10	2 S65432	angiotensin I - ho
2	41	100.0	14	2 A01250	angiotensin precu
3	41	100.0	15	2 A06834	angiotensin I prec
4	41	100.0	476	1 JC2318	angiotensin precu
5	41	100.0	477	1 ANRT	angiotensin precu
6	41	100.0	477	1 A29978	angiotensin precu
7	41	100.0	485	1 ANHU	angiotensin precu
8	41	100.0	540	2 S72233	transcription fact
9	40	97.6	10	2 A06624	angiotensin I - Ja
10	40	97.6	10	2 A90917	angiotensin precu
11	40	97.6	10	2 A90345	angiotensin precu
12	39	95.1	11	2 S07207	Crinia-angiotensin
13	37	90.2	625	1 TEB0	thrombin (EC 3.4.2
14	36	87.8	277	2 E86229	hypothetical prote
15	36	87.8	289	2 C96610	hypothetical prote
16	35	85.4	305	2 D69362	tRNA intron endonu
17	35	85.4	1355	1 VGBE11	149K glycoprotein
18	34	82.9	128	2 G81220	hypothetical prote
19	34	82.9	132	2 F82800	hypothetical prote
20	34	82.9	316	2 T34838	probable transfera
21	34	82.9	481	2 S76115	hypothetical prote
22	33	80.5	56	2 H82647	hypothetical prote
23	33	80.5	178	2 B42845	3-hydroxybutyrate
24	33	80.5	221	2 A86163	protein F15K9.22 [
25	33	80.5	559	2 A12227	hypothetical prote
26	33	80.5	617	2 S10511	hypothetical prote
27	33	80.5	622	1 TBHU	thrombin (EC 3.4.2
28	33	80.5	681	2 I78558	hypothetical Brach
29	33	80.5	695	1 S05008	complement subcomp

30	33	80.5	695	2 T24950	hypothetical prote
31	33	80.5	736	2 D86271	protein F16A14.2 [
32	33	80.5	1062	2 H83966	carbamoyl-phosphat
33	33	80.5	1063	2 T46284	hypothetical prote
34	33	80.5	1071	2 F39845	carbamoyl-phosphat
35	33	80.5	1076	2 A69409	carbamoyl-phosphat
36	33	80.5	1095	2 T13964	probable histone d
37	33	80.5	3971	2 T44806	mycosubtilin synth
38	32	78.0	105	1 FETWT	ferredoxin [3Fe-4S
39	32	78.0	177	2 C71329	hypothetical prote
40	32	78.0	223	2 AGL166	Ribulose-5-phospha
41	32	78.0	230	2 E69233	carbamoyl-phosphat
42	32	78.0	263	2 F84339	hypothetical prote
43	32	78.0	301	2 D64938	hypothetical prote
44	32	78.0	301	2 A99940	hypothetical prote
45	32	78.0	301	2 E85788	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432  
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Ridling, G.; Kemp, D.; Willadsen

Eur. J. Biochem. 237, 414-423, 1996  
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipt  
A:Reference number: S65431; MUID:96215437  
A:Accession: S65432  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <WID>

A>Note: the source is designated as Haematobia irritans exigua

Query Match 100.0% Score 41; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7

Db 1 DRVYIHP 7

##### RESULT 2

A01250  
angiotensin precursor - horse (fragment)  
C:Species: Equus caballus (domestic horse)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998  
C:Accession: A92775; A01250  
R:Skeggis Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957  
A:Reference number: A92775  
A:Accession: A92775

A:Molecule type: protein  
A:Residues: 1-14 <SKE>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin I #status experimental <ANI>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0% Score 41; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7

Db 1 DRVYIHP 7

```
RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N:Alternate names: angiotensinogen I
N:Contains: angiotensin I
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C:Accession: A60834
R:Oliver, J.A.
Hypertension 11, 21-27, 1988
A:Title: Purification and partial characterization of canine angiotensinogen.
A:Reference number: A60834; MUID:88113996
A:Accession: A60834
A:Molecule type: protein
A:Residues: 1-15 <OLI>
C:Superfamily: antithrombin III
C:Keywords: glycoprotein; plasma
F:1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 41; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.044; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 DRVYIHP 7
Db 1 DRVYIHP 7

RESULT 4
JC2318
angiotensin precursor - sheep
N:Alternate names: angiotensinogen
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JC2318; A25406
R:Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura, T. J. Biochem. 154, 597-601, 1986
A:Title: Sequencing and expression of sheep angiotensinogen cDNA.
A:Reference number: JC2318; MUID:95072318
A:Accession: JC2318
A:Molecule type: mRNA
A:Residues: 1-476 <NAG>
A:Cross-references: DDBJ:D17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183
A:Experimental source: liver
A:Note: the authors translated the codon TTC for residue 465 as Leu
R:Fernley, R.F.; John, M.; Niall, H.D.; Coghlan, J.P.
A:Title: Purification and characterization of ovine angiotensinogen.
A:Reference number: A25406; MUID:86136099
A:Accession: A25406
A:Molecule type: protein
A:Residues: 23-37, X', 39 <PER>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:24-476/Product: angiotensinogen #status predicted <MPT>
F:25-34/Product: angiotensin #status predicted <MAT>
F:295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 41; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7
Db 25 DRVYIHP 31

RESULT 5
ANRT
angiotensin precursor - rat
N:Contains: angiotensin I; angiotensin II; angiotensin III
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C:Accession: A93945; A90456; A01251
R:Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A:Title: Cloning and sequence analysis of cDNA for rat angiotensinogen.
A:Reference number: A93945; MUID:83169849
A:Accession: A93945
A:Molecule type: mRNA
A:Residues: 1-477 <OH>
A:Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A:Title: Rat angiotensinogen and Des(antiotensin)angiotensinogen: purification, char
A:Reference number: A90456; MUID:82091819
A:Accession: A90456
A:Molecule type: protein
A:Residues: 25-41 <BOU>
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C:Comment: the release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1 angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MPT>
F:25-34/Product: angiotensin I #status experimental <PPI>
F:25-32/Product: angiotensin II #status experimental <PP2>
F:26-32/Product: angiotensin III #status experimental <PP3>
F:295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 41; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7
Db 25 DRVYIHP 31

RESULT 6
A29978
angiotensin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A29978
R:Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
Genomics 2, 240-248, 1988
A:Title: Molecular cloning of the mouse angiotensinogen gene.
A:Reference number: A29978; MUID:88284703
A:Accession: A29978
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-477 <CLO>
A:Cross-references: GB:AF045887; GB:J03046; NID:g2842773; PIDN:AAC01765.1; PID:g28427
C:Genetics:
C:Introns: 277/1; 366/2; 414/3
C:Superfamily: antithrombin III
C:Keywords: blood pressure control
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MAT>

Query Match 100.0%; Score 41; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7
```

Db 25 DRVYIHP 31  
|||||||

## RESULT 7

ANNU

angiotensin precursor [validated] - human  
N:Alternate names: angiotensinogen  
N:Contains: angiotensin I; angiotensin II; angiotensin III  
C:Species: Homo sapiens (man)  
C:Date: 06-Jul-1982 #sequence\_revision 19-Jan-1996 #text\_change 08-Dec-2000  
C:Accession: A35203; I37168; I37169; A60825; I39462; A90226; I54281; A01  
R:Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami, J. Biol. Chem. 265, 7576-7582, 1990  
A:Title: Structure and expression of the human angiotensinogen gene. Identification of a  
A:Reference number: A35203; MUID:90237063  
A:Accession: A35203  
A:Molecule type: DNA  
A:Residues: 1-485 <FUK>  
C:Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327  
Gallard, I.; Clauser, E.; Corvol, P.  
DNA 8, 87-99, 1989  
A:Title: Structure of human angiotensinogen gene.  
A:Reference number: A31362; MUID:89170129  
A:Accession: A31362  
A:Molecule type: DNA  
A:Residues: 1-267, 'M', 269-332, 'E', 334-485 <GAI>  
A:Cross-references: GB:M24686; GB:M24687; GB:M24688  
A:Note: the authors translated the codon GAA for residue 333 as Gln  
R:Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.  
J. Biol. Chem. 269, 28598-28605, 1994  
A:Title: Identification of cell type-dependent enhancer core element located in the 3'-  
A:Reference number: I37168; MUID:95050659  
A:Accession: I37168  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-285 <NIB1>  
A:Cross-references: EMBL:X15324; NID:g1197496; PIDN:CAA33385.1; PID:g1197497  
A:Accession: I37169  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 287-375 <NIB2>  
A:Cross-references: EMBL:X15325; NID:g28695  
R:Kunapuli, S.P.; Benedict, C.R.; Kumar, A.  
Arch. Biochem. Biophys. 254, 642-646, 1987  
A:Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.  
A:Reference number: A60825; MUID:87212053  
A:Accession: A60825  
A:Molecule type: mRNA  
R:Kunapuli, S.P.; Kumar, A.  
Circ. Res. 60, 786-790, 1987  
A:Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence of  
A:Reference number: I39462; MUID:87244745  
A:Accession: I39462  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-267, 'M', 269-338 <KUN>  
A:Cross-references: GB:M69110; NID:g178643; PIDN:AAA52282.1; PID:g553181  
R:Kageyama, R.; Ohkubo, H.; Nakanishi, S.  
Biochemistry 23, 3603-3609, 1984  
A:Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequ  
A:Reference number: A90487; MUID:85000455  
A:Accession: A90487  
A:Molecule type: mRNA  
A:Residues: 1-267, 'M', 269-485 <KAG>  
A:Cross-references: GB:K02215; NID:g178639; PIDN:AAA51731.1; PID:g178640  
A:Note: it is uncertain whether Met-1 or Met-10 is the initiator  
R:Teaksbury, D.A.; Dart, R.A.; Travis, J.  
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981  
A:Title: The amino terminal amino acid sequence of human angiotensinogen.  
A:Reference number: A90226; MUID:81255848  
A:Accession: A90226

A:Molecule type: protein  
A:Residues: 34-46, 'X', 48-50, 'S', 52-57, 'D' <TEW>  
R:Hixson, J.E.; Powers, P.K.  
Hum. Genet. 96, 110-112, 1995  
A:Title: Detection and characterization of new mutations in the human angiotensinogen  
A:Reference number: I54281; MUID:95331754  
A:Accession: I54281  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 176-241, 'I', 243-267, 'M', 269-287, 'ANLSAG' <HTX>  
A:Cross-references: GB:S78529; NID:9999316; PIDN:AA014287.1; PID:g4261987  
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted  
e I (angiotensin-converting enzyme), primarily in the lungs.  
C:Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and  
sp-11angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.  
C:Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels,  
o induces thirst.  
C:Comment: Angiotensin II and angiotensin III are equally potent in stimulating the s  
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.  
C:Genetics:  
A:Gene: GDB:AGT  
A:Cross-references: GDB:118750; OMIM:106150  
A:Map position: Iq42-Iq43  
A:Introns: 286/1; 375/2; 423/3  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor  
F:1-33/Domain: (or 10-33) signal sequence #status predicted <SIG>  
F:34-485/Product: angiotensinogen #status predicted <MPT>  
F:34-43/Product: angiotensin I #status experimental <PPI>  
F:34-41/Product: angiotensin II #status experimental <PP2>  
F:35-41/Product: angiotensin III #status experimental <PP3>  
F:47,170,304,328/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 41; DB 1; Length 485;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYIHP 7  
Db 34 DRVYIHP 40  
RESULT 8  
S72233  
transcription factor tbx6 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C:Accession: S72233; S72232  
R:Agulnik, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: S72233  
A:Accession: S72233  
A:Molecule type: mRNA  
A:Residues: 1-540 <AGU>  
A:Cross-references: EMBL:U57331; NID:g1620601; PIDN:AAC53110.1; PID:g1620602  
R:Agulnik, S.I.; Garvey, N.; Hancock, S.; Ruvinsky, I.; Chapman, D.L.; Agulnik, I.; B  
Genetics 144, 249-254, 1996  
A:Title: Evolution of mouse T-box genes by tandem duplication and cluster dispersion.  
A:Reference number: S72230; MUID:97032942  
A:Accession: S72232  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 100-280 <AGW>  
A:Cross-references: EMBL:U57331  
C:Genetics:  
A:Gene: tbx6  
C:Superfamily: T-box homology  
C:Keywords: DNA binding  
F:100-282/Domain: T-box homology <TBX>  
Query Match 100.0%; Score 41; DB 2; Length 540;

Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 170 DRVYIHP 176

RESULT 9  
A0624  
angiotensin I - Japanese quail  
C:Species: Coturnix coturnix Japonica (Japanese quail)  
C:Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-May-1999  
C:Accession: A0624  
R:Takei, Y.; Hasegawa, Y.  
Gen. Comp. Endocrinol. 79, 12-22, 1990  
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of these effects by angiotensin II  
A:Reference number: A0624; MUID:90284684  
A:Accession: A0624  
A:Molecule type: protein  
A:Residues: 1-10 <TAK>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 97.6%; Score 40; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.045;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 1 DRVYVHP 7

RESULT 10  
A0917  
angiotensin precursor - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A0917; A01250  
R:Nakayama, T.; Nakajima, T.; Sokabe, H.  
Chem. Pharm. Bull. 21, 2085-2087, 1973  
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its precursor  
A:Reference number: A0917; MUID:74127845  
A:Accession: A0917  
A:Molecule type: protein  
A:Residues: 1-10 <NAK>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
C:1-10/Product: angiotensin I #status experimental <AN1>  
C:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.6%; Score 40; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.045;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 1 DRVYVHP 7

RESULT 11  
A0345  
angiotensin precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 20-Mar-1998  
C:Accession: A0345; A01250  
R:Elliot, D.F.; Peart, W.S.  
Biochem. J. 65, 246-254, 1957  
A:Title: The amino acid sequence in a hypertensin.  
A:Reference number: A0345  
A:Accession: A0345  
A:Molecule type: protein

A:Residues: 1-10 <ELL>  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
C:1-10/Product: angiotensin I #status experimental <AN1>  
C:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.6%; Score 40; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.045;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
|||||  
Db 1 DRVYVHP 7

RESULT 12  
S07207  
Crinia-angiotensin, skin - frog (Crinia georgiana)  
C:Species: Crinia georgiana  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Aug-2000  
C:Accession: S07207  
R:Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.  
Experientia 35, 1132-1133, 1979  
A:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II precursor  
A:Reference number: S07207; MUID:80024575  
A:Accession: S07207  
A:Molecule type: protein  
A:Residues: 1-11 <ERS>  
C:Superfamily: unassigned animal peptides

Query Match 95.1%; Score 39; DB 2; Length 11;  
Best Local Similarity 71.4%; Pred. No. 0.079;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
||:|:|  
Db 4 DRVYVHP 10

RESULT 13  
TB80  
thrombin (EC 3.4.21.5) precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 24-Apr-1984 #sequence\_revision 14-Jul-1994 #text\_change 18-Jun-1999  
C:Accession: S02537; A00915; A37552; I46045; S67518  
R:Irwin, D.M.; Robertson, K.A.; MacGillivray, R.T.A.  
J. Mol. Biol. 200, 31-45, 1988  
A:Title: Structure and evolution of the bovine prothrombin gene.  
A:Reference number: S02537; MUID:88245190  
A:Accession: S02537  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-625 <IRW>  
R:MacGillivray, R.T.A.; Davie, E.W.  
Biochemistry 23, 1626-1634, 1984  
A:Title: Characterization of bovine prothrombin mRNA and its translation product.  
A:Reference number: A00915; MUID:84203525  
A:Accession: A00915  
A:Molecule type: mRNA  
A:Residues: 1-230, 'H', 232-625 <MAC>  
A>Note: 600-Asn was also found  
R:Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys, H.  
in Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C.,  
ed., 1984, pp. 1-10  
A:Reference number: A37552  
A:Accession: A37552  
A:Molecule type: protein  
A:Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625 <MAG>  
A>Note: the evidence for 231-Ser is strong  
A>Note: disulfide bonds and carbohydrate binding sites were determined  
R:Park, C.H.; Tulinsky, A.  
Biochemistry 25, 3977-3982, 1986  
A:Title: Three-dimensional structure of the kringle sequence: structure of prothrombin



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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:39:14 ; Search time 34.05 Seconds  
(without alignments)  
7.960 Million cell updates/sec

Title: US-09-723-197-4  
Perfect score: 41  
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues 105224  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
2	41	100.0	14	1 ANGT_HORSE	P01016 equus cabal
3	41	100.0	436	1 TBX6_HUMAN	O95947 homo sapien
4	41	100.0	476	1 ANGT_SHEEP	P20757 ovis aries
5	41	100.0	477	1 ANGT_MOUSE	P11859 mus musculus
6	41	100.0	477	1 ANGT_RAT	P01015 rattus norv
7	41	100.0	485	1 ANGT_HUMAN	P01019 homo sapien
8	41	100.0	540	1 TBX6_MOUSE	P70327 mus musculus
9	40	97.6	10	1 ANGL_BOTJA	Q10581 bothrops ja
10	40	97.6	10	1 ANGT_BOVIN	P01017 bos taurus
11	40	97.6	10	1 ANGT_CHICK	P01018 gallus gall
12	39	95.1	11	1 ANGT_CRIGE	P09037 crinia geor
13	37	90.2	625	1 THRB_BOVIN	P09035 bos taurus
14	35	85.4	305	1 ENDA_ARCFU	O29362 archaeoglob
15	35	85.4	501	1 TX18_HUMAN	O70306 mus musculus
16	35	85.4	602	1 TX15_MOUSE	Q9epz6 mus musculus
17	35	85.4	613	1 TX18_MOUSE	Q00104 ictalurid h
18	35	85.4	1355	1 VG46_HSV1	Q55587 synechocyst
19	34	82.9	481	1 Y335_SYNY3	P24043 homo sapien
20	34	82.9	3110	1 LMA2_HUMAN	Q02337 bos taurus
21	33	80.5	178	1 BDH_BOVIN	O62589 drosophila
22	33	80.5	528	1 GD_DROME	P18292 rattus norv
23	33	80.5	617	1 THRB_RAT	P00734 homo sapien
24	33	80.5	622	1 THRB_HUMAN	Q64336 mus musculus
25	33	80.5	681	1 TBR1_HUMAN	Q16650 homo sapien
26	33	80.5	682	1 TBR1_HUMAN	P15156 mesocricetu
27	33	80.5	695	1 CASP_MESAU	P25994 bacillus su
28	33	80.5	1071	1 CARB_BACSU	Q922v5 mus musculus
29	33	80.5	1149	1 HDAG_MOUSE	Q9ubn7 homo sapien
30	33	80.5	1215	1 HDAG_HUMAN	P03942 thermus aqu
31	32	78.0	78	1 FER_THETH	O83419 treponema p
32	32	78.0	177	1 Y404_TREPA	P39173 escherichia
33	32	78.0	294	1 UP08_ECOLI	

34	32	78.0	378	1 EXT1_CAEEL	O01704 caenorhabdi
35	32	78.0	414	1 TBX3_CHICK	O73718 gallus gall
36	32	78.0	427	1 AROA_AERPE	O9yek9 aeropyrum p
37	32	78.0	482	1 NCAP_CCHFV	P27317 crimean-con
38	32	78.0	485	1 NCAP_HAZVJ	P27318 hazara viru
39	32	78.0	535	1 TX21_HUMAN	O9ul17 homo sapien
40	32	78.0	618	1 THRB_MOUSE	P19221 mus musculu
41	32	78.0	692	1 EOMD_XENLA	P79944 xenopus lae
42	32	78.0	701	1 TBX2_MOUSE	Q60707 mus musculu
43	32	78.0	702	1 TBX2_HUMAN	Q13207 homo sapien
44	32	78.0	721	1 NICA_CAEEL	Q23316 caenorhabdi
45	32	78.0	742	1 TBX3_HUMAN	O15119 homo sapien

ALIGNMENTS

RESULT 1

ANG2\_BOTJA

ID ANG2\_BOTJA STANDARD; PRT; 8 AA.

AC Q10582;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Angiotensin-like peptide II (Fragment)

OS Bothrops jararaca (Jararaca)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8724;

RN [1]

RP SEQUENCE.

RC TISSUE=Plasma;

RX MEDLINE=96208932; PubMed=8829801;

RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

RT "Isolation and identification of angiotensin-like peptides from the

RT plasma of the snake Bothrops jararaca."

RL Comp. Biochem. Physiol. 113B:467-473(1996).

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR InterPro: IPR000215; Serpin.

DR PROSITE: PS00284; SERPIN; PARTIAL.

KW Vasoconstrictor; Plasma; Serpin.

FT NON\_TER 8 8

SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match

Best Local Similarity 100.0%; Score 41; DB 1; Length 8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7

Db 1 DRVYIHP 7

RESULT 2

ANGT\_HORSE

ID ANGT\_HORSE STANDARD; PRT; 14 AA.

AC P01016;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Angiotensinogen (Contains: Angiotensin I; Angiotensin II) (Fragment).

GN SERPIN8 OR AGT.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE.

RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;

RT "The preparation, purification, and amino acid sequence of a

RT polypeptide renin substrate."

J. Exp. Med. 106:439-453(1957).

-1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.

-1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

PIR: A01250; A01250.

InterPro: IPR000215; Serpin.

PROSITE: PS00284; SERPIN; PARTIAL.

Vasodilator; Plasma; Serpin.

PEPTIDE 1 10 ANGIOTENSIN I.

NON\_TER 1 8 ANGIOTENSIN II.

SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBD7 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7  
Db 1 DRVYIHP 7

RESULT 3  
TXB6\_HUMAN  
ID TXB6\_HUMAN STANDARD; PRT; 436 AA.  
AC O95947;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX6 (T-box protein 6).  
GN TBX6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99134303; PubMed=9933572;  
RA Papapetrou C., Putt W., Fox M., Edwards Y.H.;  
RT "The human TBX6 gene: Cloning and assignment to chromosome 16p11.2.";  
RL Genomics 55:238-241(1999).  
RN [2]  
RP SEQUENCE OF 135-272 FROM N.A.  
RX TISSUE=Myeloid;  
RA MEDLINE=99107806; PubMed=9888994;  
RA Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,  
RA Anstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;  
RT "Identification, mapping and phylogenomic analysis of four new human members of the T-box gene family: BOMES, TBX6, TBX18, and TBX19.";  
RL Genomics 55:10-20(1999).  
RN [1]  
RP FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).  
RN [2]  
RP SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).  
RN [3]  
RP SUBCELLULAR LOCATION: Nuclear (potential).  
RN [4]  
RP TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL TISSUE, INTERVERTEBRAL DISC AND TESTIS, ALSO EXPRESSED IN ADULT TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.  
RN [5]  
RP DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A SECOND PHASE IN SOME ADULT TISSUES.  
RN [6]  
RP SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

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EMBL: AJ007989; CAA07812.1;  
EMBL: AJ010279; CAB37938.1;  
HSSP: P24781; IYBR.  
MIM: 602427;  
InterPro: IPR001699; T-box.  
Pfam: PF00907; T-box; 1.  
PRINTS: PR00937; TBOX.  
SMART: SM00425; TBOX; 1.  
PROSITE: PS01283; TBOX\_1; 1.  
PROSITE: PS01284; TBOX\_2; 1.  
PROSITE: PS0252; TBOX\_3; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein;  
Developmental protein.  
DVA\_BIND 100 273 T-BOX.  
FT CONFLICT 207 207 H -> HV (IN REF. 2).  
SQ SEQUENCE 436 AA; 47017 MW; 438178BD31B966E9 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7  
Db 170 DRVYIHP 176

RESULT 4  
ANGT\_SHEEP  
ID ANGT\_SHEEP STANDARD; PRT; 476 AA.  
AC P20757;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPIN A8 OR AGT.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RA MEDLINE=95072318; PubMed=7765514;  
RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,  
RA Murakami K., Nakamura Y.;  
RT "Sequencing and expression of sheep angiotensinogen cDNA.";  
RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).  
RN [2]  
RP SEQUENCE OF 25-39.  
RX MEDLINE=86136099; PubMed=3081342;  
RA Fernley R.F., John M., Niall H.D., Coghlan J.P.;  
RT "Purification and characterization of ovine angiotensinogen.";  
RL Eur. J. Biochem. 154:597-601(1986).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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CC -----
CC DR EMBL: D17520; BAA04470.1; -
CC DR PIR: A25406; A25406.
CC DR InterPro: IPR000227; Angiotensngn.
CC DR Pfam: PF00079; serpin.1.
CC DR PRINTS: PR00654; ANGIOTENSNGN.
CC DR SMART: SM00093; SERPIN.1.
CC DR PROSITE: PS00284; SERPIN.1.
CC KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 476 ANGIOTENSINOGEN.
CC FT PEPTIDE 25 34 ANGIOTENSIN I.
CC FT PEPTIDE 25 32 ANGIOTENSIN II.
CC FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7
Db 25 DRVYIHP 31
|||||

RESULT 5
ANGT_MOUSE STANDARD; PRT; 477 AA.
ID ANGT_MOUSE
AC P11859;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN SERPINB8 OR AGT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
ON NCBI_TaxID=10090;
RX SEQUENCE FROM N.A.
RX MEDLINE=88284703; PubMed=3397061;
RA Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT "Molecular cloning of the mouse angiotensinogen gene.";
RL Genomics 2:240-248(1988).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC DR EMBL: AF045887; AAC01765.1; -
CC DR EMBL: AF045886; AAC01765.1; JOINED.
CC DR EMBL: AF045885; AAC01765.1; JOINED.
CC DR EMBL: AF045884; AAC01765.1; JOINED.
CC DR PIR: A29978; A29978.
CC MGI: 87963; Agt.
CC InterPro: IPR000227; Angiotensngn.
CC DR Pfam: PF00079; serpin.1.

PRINTS; PR00654; ANGIOTENSNGN.
SMART: SM00093; SERPIN.1.
PROSITE: PS00284; SERPIN; FALSE_NEG.
Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 477 ANGIOTENSINOGEN.
FT PEPTIDE 25 34 ANGIOTENSIN I.
FT PEPTIDE 25 32 ANGIOTENSIN II.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 477 AA; 51990 MW; A877F4029F338607 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7
Db 25 DRVYIHP 31
|||||

RESULT 6
ANGT_RAT STANDARD; PRT; 477 AA.
ID ANGT_RAT
AC P01015;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN SERPINA8 OR AGT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX SEQUENCE FROM N.A.
RX STRAIN=Wistar;
RX MEDLINE=83169849; PubMed=6572971;
RA Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA Nakanishi S.;
RT "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN [1]
CC SEQUENCE OF 25-34.
CC MEDLINE=73060322; PubMed=4344907;
CC Nakayama T., Nakajima T., Sokabe H.;
CC "Comparative studies on angiotensins. II. Structure of rat
CC angiotensin and its identification by DNS-method.";
CC Chem. Pharm. Bull. 20:1579-1581(1972).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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DR InterPro; IPR000227; Angiotensngn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; FALSE\_NEG.  
KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 477 ANGIOTENSIN I.  
FT PEPTIDE 25 34 ANGIOTENSIN II.  
FT PEPTIDE 25 32 ANGIOTENSIN II.  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 477 AA; 51981 MW; 689051A5788D693D CRC64;

Query Match 100.0%; Score 41; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 DRVYHP 7  
|||||  
25 DRVYHP 31

DB

RESULT 7  
ANGT\_HUMAN STANDARD; PRT; 485 AA.  
ID AC P01019; Q16358; Q16359.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].  
GN SERPINA8 OR AGT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89170129; PubMed=2924688;  
RA Gallard I., Clauser E., Corvol P.;  
RT "Structure of human angiotensinogen gene.";  
RL DNA 8:87-99(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85000455; PubMed=6089875;  
RA Kageyama K., Ohkubo H., Nakanishi S.;  
RT "Primary structure of human preangiotensinogen deduced from the  
cloned cDNA sequence.";  
RL Biochemistry 23:3603-3609(1984).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90237063; PubMed=1692023;  
RA Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,  
RA Murakami K.;  
RT "Structure and expression of the human angiotensinogen gene.  
Identification of a unique and highly active promoter.";  
RL J. Biol. Chem. 265:7576-7582(1990).  
RN [4]  
RP SEQUENCE OF 1-338 FROM N.A.  
RX MEDLINE=87244745; PubMed=2885106;  
RA Kunapuli S.P., Kumar A.;  
RT "Molecular cloning of human angiotensinogen cDNA and evidence for the  
presence of its mRNA in rat heart.";  
RL Circ. Res. 60:786-790(1987).  
RN [5]  
RP SEQUENCE OF 34-45, AND SUBUNITS.  
RC TISSUE-Serum;  
RX MEDLINE=95293954; PubMed=7539791;  
RA Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,  
RA Stigbrand T., Gleich G.J., Sottrup-Jensen L.;  
RT "Identification of angiotensinogen and complement C3dg as novel

proteins binding the proform of eosinophil major basic protein in  
human pregnancy serum and plasma.";  
J. Biol. Chem. 270:13645-13651(1995).  
RN [6]  
RP SEQUENCE OF 34-43.  
RX MEDLINE=6904170; PubMed=4300938;  
RA Arakawa K., Minohara A., Yamada J., Nakamura M.;  
RT "Enzymatic degradation and electrophoresis of human angiotensin I.";  
Biochim. Biophys. Acta 168:106-112(1968).  
RN [7]  
RP STRUCTURE BY NMR OF ANGIOTENSIN II.  
MEDLINE=98151281; PubMed=9492317;  
RX Carpenter K.A., Wilkes B.C., Schiller P.W.;  
RA "The octapeptide angiotensin II adopts a well-defined structure in a  
phospholipid environment.";  
RT Eur. J. Biochem. 251:448-453(1998).  
RN [8]  
RP VARIANTS MET-207; THR-268 AND CYS-281.  
RX MEDLINE=93008239; PubMed=1394429;  
RA Jeunenaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,  
Williams C.S., Charu A., Hunt S.C., Hopkins P.N., Williams R.R.,  
Lalouel J.-M., Corvol P.;  
RA "Molecular basis of human hypertension: role of angiotensinogen.";  
Cell 71:169-180(1992).  
RN [9]  
RP VARIANT THR-268.  
RX MEDLINE=93291876; PubMed=8513325;  
RA Ward K., Hata A., Jeunenaitre X., Helin C., Nelson L., Namikawa C.,  
Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,  
Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;  
RA "A molecular variant of angiotensinogen associated with  
preeclampsia.";  
RT Nat. Genet. 4:59-61(1993).  
RN [10]  
RP VARIANTS ILE-242; ARG-244 AND CYS-281.  
RX MEDLINE=95331754; PubMed=7607642;  
RA Hixson J.E., Powers P.K.;  
RT "Detection and characterization of new mutations in the human  
angiotensinogen gene (AGT).";  
RL Hum. Genet. 96:110-112(1995).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
BALANCE OF BODY FLUIDS.  
CC -1- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2  
heterotetramer with the proform of PRG2 and as a complex (probably  
a 2:2:2 heterotrimer) with pro-PRG2 and C3dg.  
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -1- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO  
ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION  
(PIH) (PREECLAMPSIA).  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.  
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CC -----  
DR EMBL; K02215; AAA51731.1; -  
DR EMBL; M24689; AAA51679.1; JOINED.  
DR EMBL; M24686; AAA51679.1; JOINED.  
DR EMBL; M24687; AAA51679.1; JOINED.  
DR EMBL; M24688; AAA51679.1; JOINED.  
DR EMBL; X15324; CAA33385.1; -  
DR EMBL; X15325; CAA33385.1; JOINED.  
DR EMBL; X15326; CAA33385.1; JOINED.  
DR EMBL; X15327; CAA33385.1; JOINED.

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DR EMBL; M69110; AAA52282.1; -
DR EMBL; S78529; AAD14287.1; -
DR EMBL; S78530; AAD14288.1; -
DR PIR; A01249; ANHU.
DR PIR; A31362; A31362.
DR PIR; A35203; A35203.
DR SWISS-2DPAGE; P01019; HUMAN.
DR MIM; 106150; -.
DR InterPro; IPR000227; Angiotensngn.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PRINTS; PR00654; ANGIOTENSNGN.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
KW Disease mutation; Polymorphism.
FT SIGNAL 1 33
FT CHAIN 34 485
FT PEPTIDE 34 43
FT PEPTIDE 34 41
FT CARBOHYD 47 47
FT CARBOHYD 170 170
FT CARBOHYD 304 304
FT CARBOHYD 328 328
FT VARIANT 207 207
FT VARIANT 242 242
FT VARIANT 244 244
FT VARIANT 268 268
FT VARIANT 281 281
FT CONFLICT 333 333
FT SEQUENCE 485 AA; 53154 MW; 5026C2DFB2DD236E CRC64;

Query Match 100.0%; Score 41; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 DRVYIHP 7
Db 34 DRVYIHP 40
|||||

RESULT 8
TX6_MOUSE STANDARD; PRT; 540 AA.
AC P70327;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-box transcription factor TBX6 (T-box protein 6).
GN TBX6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97032942; PubMed=8878690;
RA Aguilnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,
RA Aguilnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;
RT Evolution of mouse T-box genes by tandem duplication and cluster
RT dispersion."
RL Genetics 144:249-254(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastrula;
RX MEDLINE=97115702; PubMed=8954725;
```

```
RA Chapman D.L., Aguilnik I., Hancock S., Silver L.M., Papaioannou V.E.;
RT "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at
RT gastrulation."
RL Dev. Biol. 180:534-542(1996).
RN [3]
RP FUNCTION.
RX MEDLINE=98140705; PubMed=9490412;
RA Chapman D.L., Papaioannou V.E.;
RT "Three neural tubes in mouse embryos with mutations in the T-box gene
RT Tbx6."
RL Nature 391:695-697(1998).
CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL
CC MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS
CC DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL
CC PATHWAY.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION
CC STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL
CC MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,
CC PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK
CC AS THE SOURCE OF MESODERM.
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57331; AAC53110.1; -
DR HSP; P24781; IYBR.
DR MGD; MGI:102539; Tbx6.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein.
FT DOMAIN 61 64 POLY-ALA.
FT DOMAIN 79 82 POLY-PRO.
FT DOMAIN 100 273 T-BOX.
FT SEQUENCE 540 AA; 58628 MW; BC834CE2745E8E61 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 DRVYIHP 7
Db 170 DRVYIHP 176
|||||

RESULT 9
ANGL_BOTJA STANDARD; PRT; 10 AA.
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
```

RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.; the  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RL plasma of the snake Bothrops jararaca";  
 CC Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 97.6%; Score 40; DB 1; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 0.025;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 DRVYIHP 7  
 |||||  
 1 DRVYVHP 7

RESULT 10  
 ANGT\_BOVIN  
 ID ANGT\_BOVIN STANDARD; PRT; 10 AA.  
 AC P01017;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN A8 OR AGT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RA Elliott D.F., Peart W.S.;  
 RT "The amino acid sequence in a hypertensin.";  
 RL Biochem. J. 65:246-254(1957).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A01250;  
 DR PIR; A90345; A90345.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1282 MW; CEFBDD761F2DB42 CRC64;

Query Match 97.6%; Score 40; DB 1; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 0.025;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 DRVYIHP 7  
 |||||  
 1 DRVYVHP 7

RESULT 11  
 ANGT\_CHICK

ID ANGT\_CHICK STANDARD; PRT; 10 AA.  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).  
 GN SERPIN A8 OR AGT.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 93934;  
 RN [1]  
 RP SEQUENCE.

RC SPECIES=Chicken;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sokabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of fowl  
 RT angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RN [2]  
 RP SEQUENCE.

RC SPECIES=C.c.japonica;  
 RX MEDLINE=90284684; PubMed=2191893;  
 RA Takei Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and  
 RT inhibition of these effects in the Japanese quail.";  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A01250;  
 DR PIR; A90317; A90917.  
 DR PIR; A60624; A60624.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; CEFBDD761F2DB42 CRC64;

Query Match 97.6%; Score 40; DB 1; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 0.025;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHP 7  
 |||||  
 DB 1 DRVYVHP 7

RESULT 12  
 ANGT\_CRIGE  
 ID ANGT\_CRIGE STANDARD; PRT; 11 AA.  
 AC P09037;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Crinia angiotensin II.  
 OS Crinia georgiana (Quacking frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Crinia.  
 OX NCBI\_TaxID=8374;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=SKIN;  
RX MEDLINE=80024575; PubMed=488254;  
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Edean R.;  
RT "Amino acid composition and sequence of crinia-angiotensin, an  
RT angiotensin II-like endopeptide from the skin of the Australian  
RT frog Crinia georgiana.";  
RL Experientia 35:1132-1133(1979).  
DR PIR; S07207; S07207.  
KW Vasoconstrictor.  
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 95.1%; Score 39; DB 1; Length 11;  
Best Local Similarity 71.4%; Pred. No. 0.044;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYHP 7  
||:|:|  
Db 4 DRVYHP 10

RESULT 13  
THRB\_BOVIN STANDARD; PRT; 625 AA.  
AC P00735;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Prothrombin precursor (EC 3.4.21.5).  
GN F2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88245190; PubMed=3379642;  
RA Irwin D.M., Robertson K.A., Macgillivray R.T.A.;  
RT "Structure and evolution of the bovine prothrombin gene.";  
RL J. Mol. Biol. 200:31-45(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84203525; PubMed=6326805;  
RA Macgillivray R.T.A., Davie E.W.;  
RT "Characterization of bovine prothrombin mRNA and its translation  
RT product.";  
RL Biochemistry 23:1626-1634(1984).  
RN [3]  
RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.  
RA Magnusson S., Sottrup-Jensen L., Petersen T.E., Claess H.;  
RL (In) Hemker H.C., Velkamp J.J. (eds.);  
RL Boerhaave symposium on prothrombin and related coagulation factors,  
RL pp.25-46, Leiden University Press, Leiden (1975).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
RX MEDLINE=86296631; PubMed=3741841;  
RA Park C.H., Tulinsky A.;  
RT "Three-dimensional structure of the kringle sequence: structure of  
RT prothrombin fragment 1.";  
RL Biochemistry 25:3977-3982(1986).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
RX MEDLINE=91311686; PubMed=1856865;  
RA Seshadri T.P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;  
RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A  
RT resolution.";  
RL J. Mol. Biol. 220:481-494(1991).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.  
RX MEDLINE=92190185; PubMed=1547238;  
RA Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;  
RT "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-

RT prothrombin fragment 1.";  
RL Biochemistry 31:2554-2566(1992).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RX MEDLINE=92218459; PubMed=1560020;  
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;  
RT "The structure of residues 7-16 of the A alpha-chain of human  
RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";  
RL J. Biol. Chem. 267:7911-7920(1992).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RX MEDLINE=92389319; PubMed=1518046;  
RA Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,  
RA Martin P.D., Edwards B.F.P., Bode W.;  
RT "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes  
RT formed with the benzamidine and arginine-based thrombin inhibitors  
RT NAPAP, 4-TAPAP and MQPA. A starting point for improving  
RT antithrombotics.";  
RL J. Mol. Biol. 226:1085-1089(1992).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.  
RX MEDLINE=97102783; PubMed=8947023;  
RA van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,  
RA Hoeffken W., Huber R.;  
RT "The ornithodorin-thrombin crystal structure, a key to the TAP  
RT enigma?";  
RL EMBO J. 15:6011-6017(1996).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.  
RX MEDLINE=98004486; PubMed=9342325;  
RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,  
RA Huber R., Bode W.;  
RT "Structure of the thrombin complex with triabin, a lipocalin-like  
RT exosite-binding inhibitor derived from a triatomine bug.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).  
RN [11]  
RP GENE STRUCTURE.  
RX MEDLINE=86077733; PubMed=3000440;  
RA Irwin D.M., Ahern K.G., Pearson G.D., Macgillivray R.T.A.;  
RT "Characterization of the bovine prothrombin gene.";  
RL Biochemistry 24:6854-6861(1985).  
RN [12]  
RP FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS  
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,  
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.  
CC  
CC -1- SUBCELLULAR LOCATION: Extracellular.  
CC  
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.  
CC  
CC -1- PPM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,  
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL  
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES  
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY  
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION  
CC OF PROTHROMBIN TO THROMBIN.  
CC  
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A  
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &  
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS. FACTOR XA REMOVES  
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &  
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR  
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF  
CC THROMBIN.  
CC  
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL  
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION  
CC BY FACTOR XA.  
CC  
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.  
CC  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
CC  
CC -1- DATABASE: NAME=Prozyme technical fact sheet;  
CC WWW="http://www.prozyme.com/technical/thrombindata.html".  
CC  
CC  
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Best Local Similarity 57.1%; Pred. No. 7.7;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYHP 7  
Db 26 DRIYHP 32

RESULT 15

TX18\_HUMAN  
ID TX18\_HUMAN STANDARD; PRT; 501 AA.  
AC O95935; Q9UJI6;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T-box transcription factor TBX18 (T-box protein 18) (Fragment).  
GN TBX18.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
PP SEQUENCE FROM N.A.  
RA Bates K.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RX SEQUENCE OF 42-223 FROM N.A.  
RA MEDLINE-99107806; PubMed-9888994;  
Yi C.-H., Terret J.A., Li Q.-Y., Ellington K., Packham E.A.,  
Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;  
RT "Identification, mapping and phylogenomic analysis of four new human  
members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";  
RL Genomics 55:10-20(1999).  
CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN  
DEVELOPMENTAL PROCESSES.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; AL035694; CAB45196.1; -  
DR EMBL; AJ010278; CAB37937.1; -  
DR HSP; P24781; 1XBR.  
DR MIM; 604613; -  
DR InterPro; IPR001699; T-box.  
DR Pfam; PF00907; T-box; 1.  
DR PRINTS; PR00937; TBOX.  
DR SMART; SM00425; TBOX; 1.  
DR PROSITE; PS01283; TBOX\_1; 1.  
DR PROSITE; PS01264; TBOX\_2; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
DR PROSITE; PS0252; TBOX\_3; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT NON\_TER 1 1  
FT DNA\_BIND 42 224 T-BOX.  
SQ SEQUENCE 501 AA; 54229 MW; 45A732B009A4E5F5 CRC64;

Query Match 85.4%; Score 35; DB 1; Length 501;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVIYHP 7  
Db 115 RVIYHP 120

Search completed: July 1, 2002, 07:47:07  
Job time: 473 sec

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